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Result
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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         length:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Gapop 60.0 ,
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa//PCTUS_COMB.pep:*
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US-08-318-837-4
US-08-326-1178-14
US-08-982-129-14
US-08-982-129-14
US-08-982-129-05-1
US-08-318-837-7
US-08-318-837-7
US-08-318-837-9
US-08-366-405-2
US-08-366-263-2
US-08-366-263-2
US-08-368-186-2
US-08-368-186-2
US-08-368-186-4
US-09-150-440-1
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PCT-US95-05512-2
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US-08-854-585-2
                                                                             Matches
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Best Local :
               324 QSRDTEVL 331
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ALIGNMENTS

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-854-585-2
                                                                                                                                                                   TELEFAX: 312-4/+ ... 2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FRUGTH: 1337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application Patent No. 6114140 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tonks, Nicholas K. and TITLE OF INVENTION: Density Enhanc NUMBER OF SEQUENCES: 6
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                                   Local Similarity hes 8; Conserv
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STATE: Illino
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1 QSRDTEVL 8
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United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, Suite 6300
                                    Conservative
                                                  100.0%;
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Pred. No.
                                   Mismatches
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0.061;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   Patent No. 5981277
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
    ZIP: 10010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE,
APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY
TITLE OF INVENTION: IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 270
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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LENGTH: 1337 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                 COUNTRY:
                                                                                                                                        STATE:
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                                                                                                                                    NEW YORK
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                                                                                                                   USA
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Sequence 4, Application ...,
Sequence 4, Application ...,
Sequence 4, Application ...,
Sequence 4, Application ...,
Patent No. 5981277

Patent No. 5981277

Patent No. 1000 ...,
COURT: APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
APPLICANT: ANDRE OF TOWN THE PIELD OF TUMOR THERAP
APPLICANT: AND THEIR USE IN THE FIELD OF TUMOR THERAP
APPLICANT: ANDRE OF TOWN THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAP

TOWN THE PIELD OF TOWN THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAP
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Best Local (
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 13-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                              COUNTRY: U:
ZIP: 10016
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CLASSIFICATION:
APPLICATION NUMBER: 92.401.231.3 FILING DATE: 30-APR-1992
                                                                                                                                                                                                           SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                          CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 DTEVL 14
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nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 28-APR-1993
                                                                                                                          CLASSIFICATION: 800
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PU5-1.8, THP-1
                                                                                                                                                                                                                                                                                                                                                                                                              BIERMAN AND MUSERLIAN
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100.0%; Pred. No.
tive 0; Mismatc
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US-08-326-117B-14
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Best Local Similarity
Watches 5; Conserva
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Patent No.
                                               Query Match
Best Local
                                Matches
                                                                                                                                                                                    TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 4:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500 TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BULLA, LEE A. APPLICANT: JI, TAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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NAME: CHARLES A. MUSERLIAN
                                                                                                                      LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: DC
                                                                                                                                                                                                                                                                             NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 7112-0037.00
                                             Local
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/326,117B FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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TOPOLOGY: linear
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o. 5693491
                              Similarity 5; Conserv
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2000 Pennsylvania Ave. N.W.
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                           62.5%; Solitarity 100.0%; I Conservative 0;
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                           s; Score 5; DB 1; Pred. No. 23; 0; Mismatches
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RESULT 7
US-08-928-443-1
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Best Local
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                                                               GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN N-ACETYL TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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APPLICANT: JI, TAE
TITLE OF INVENTION: T
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/326,117
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDLIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/982,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
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ADDRESSEE: MORRISON & FOERSTER
                                  CORRESPONDENCE ADDRESS
                                                      NUMBER OF SEQUENCES:
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TELEFAX: 90-4030
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les 5; Conservative
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TOPOLOGY: linear
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CLASSIFICATION:
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CITY: Washington
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ZIP: 20006-1812
                ADDRESSEE:
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3174 Porter Drive
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100.0%; Pred. No.
Live 0; Mismatc
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Matches
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN N-ACETYL TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 178 amino acids
                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/129,055
                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Ph
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OPERATING SYSTEM: DO:
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/928,443
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MEDIUM TYPE: Diskett
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LIBRARY: BRALL
TONE: 761783
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                  CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 62.5%; Score 5; DB:
Local Similarity 100.0%; Pred. No. 33
Nes 5; Conservative 0; Mismatches
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ZIP: 94304
                                                  CLASSIFICATION:
                                                                FILING DATE:
                                                                                                                                                                                                  ZIP: 94304
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FILING DATE:
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Best Local Similarity
"~+~hes 5; Conserva
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US-08-318-837-7
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Patent No. 5981277
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                                TELEFAX: (212) 661-8002 INFORMATION FOR SEQ ID NO: 7:
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SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acid
                                                              REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
                                                                                                                                                  APPLICATION NUMBER: PCT/EP 93/010
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92.401.231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NEW POLYPEPTIDES TITLE OF INVENTION: CODING FOR THEM, TITLE OF INVENTION: IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE, APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
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                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/318,837 FILING DATE: 13-OCT-1994
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TOPOLOGY: lin
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                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SRDTE 6
                                                                                                                                    CHARLES A. MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIERMAN AND MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%; Score 5; 1
                                                                                                                                                                                                                                            PCT/EP 93/01022
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                                                                                                                  19,683

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND PEPTIDES, NUCLEIC ACID AND THEIR USE IN THE FIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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RESULT
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Best Local Similarity luv.
""+"ches 5; Conservative
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                                                                                                               Matches
                                                                                                              Best Local Similarity
Matches 5; Conserv
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 93/01022
FILING DATE: 28-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92.401.231.3
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            TELEFAX: (212) 661-80 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN AND MUSERLIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEW POLYPEPTIDES AND PEPTIDES, NUCLEIC ACID
TITLE OF INVENTION: CODING FOR THEM, AND THEIR USE IN THE FIELD OF TUMOR THERAPY
TITLE OF INVENTION: IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FRANSEN, LUCIA; DEVOS, KATHLEEN; VAN DE VOORDE, APPLICANT: ANDRE; VAN HEUVERSWYN, HUGO
                                               193 DTEVL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 DTEVL 197
                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/318,837 FILING DATE: 13-OCT-1994 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 600 THIRD AVENUE CITY: NEW YORK
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11
                                                                             4 DTEVL 8
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100.0%; Pr
                                                                                                            62.5%; Score 5; DB;
100.0%; Pred. No. 56,
tive 0; Mismatches
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Pred. No.
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US-08-356-405-2
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                                                                                                                           GENERAL INFORMATION:
APPLICANT: Amlaiky, No. 580769:
APPLICANT: Boschert, Ursula
APPLICANT: Hen, Rene
APPLICANT: Hen, Rene
TITLE OF INVENTION: Polypeptid
TITLE OF INVENTION: Activity ()
TITLE OF INVENTION: Polypeptid
                                                                                                                                                                                                                                                           Sequence 2, Application US/08356405 Patent No. 5807691
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CM. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Construction and USe of Synthetic TITLE OF INVENTION: Constructs Encoding Syndecan
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                                                                                                               UMBER OF SEQUENCES:
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nes 5; Conserv
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COUNTRY: USA
ZIP: 19426-0107
                                 STATE:
                                                  CITY:
                                                                STREET:
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                                                                ADDRESSEE: Rhone-Poulenc Rorer STREET: 500 Arcola Road, 3C43
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                                               Collegeville
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Bernfield, Merto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617) 227-5941
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internal
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100.0%; P
tive 0;
                                                                                                                 Polypeptides and Uses Thereof
                                                                                                                                              Polypeptides Having Serotonin Receptor Activity (5HT5A), Nucleic Acids Coding for These
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COMPUTER READABLE FORM:

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US-08-806-263-2
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FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K
REGISTRATION NUMBER: 88,619
REFERENCE/DOCKET NUMBER: EX92004-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Sathe, Ganesh
APPLICANT: Van Horn, Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for I
CURRENT APPLICATION DATA:
                                                                                                                                APPLICATION NUMBER: US/0. FILING DATE: 24-FEB-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Van Horn, Stephanie
TITLE OF INVENTION: cDNA Clone HDPBI30 That Encodes
TITLE OF INVENTION: A No. 6221627el Human 7-Transmembrane Receptor
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ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                       STREET: 709 Swedeland CITY: King of Prussia
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FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                             FILING DATE:
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nes 5; Conserva
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                                                                                                                 APPLICATION NUMBER:
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for Windows Version 2.0
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                     GH50003
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o. 63;
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-969-815-4
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US-08-969-815-4
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Patent No. 6207412
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Best Local Similarity 100.
Query Match
Best Local Similarity
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                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Witte, Owen N.
APPLICANT: Weng, Zhigang
TITLE OF INVENTION: IDENTIFICATION OF A G PROTEIN-COUPLED
TITLE OF INVENTION: RECEPTOR TRANSCRIPTIONALLY REGULATED BY PROTEIN
TITLE OF INVENTION: TYROSINE KINASE SIGNALING IN HEMATOPOIETIC CELLS
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEPHAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                 LENGTH: 380 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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TELEFAX: 610-270-4026
                                                                                                                 TOPOLOGY:
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62.5%;
100.0%;
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 Score 5;
Pred. No.
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Search completed: August 31, 2002, 12:20:20 Job time: 135 sec
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US-09-120-025-4
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SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                            Query Match 62.5%; Score 5; DB 4; Best Local Similarity 100.0%; Pred. No. 67; Matches 5; Conservative 0; Mismatches
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Patent No. 6214562
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/969,815
APPLICATION NUMBER: 08/969,815
FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: UCLA015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEPHONE: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT: Witte, Owen N.
TITLE OF INVENTION: TRANSCRIPTIONALLY REGULATED G PROTEIN-COUPLED
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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341 SRDTE 345
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STATE: CA
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Perfect score:
Sequence:
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Maximum
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length:
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Match
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                                                                                                                                                                                                                                                                   Length
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          GenCore version (c) 1993 - 2000
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 CPDF_CANFA
CPDF_CANFA
CPDF_CANFA
CPDG_CAVPO
P518_HUMAN
E189_ADE07
VH07_VACCV
VH07_VACCC
GLBD_CAUAR
PUR1_LACCA
VNS3_AHSV4
ISPD_CHLTR
PYRE_KIJULA
YWFC_BACSU
DHSB_ECOLI
RL5_DUNSA
YWFC_BACSU
DHSB_ECOLI
RL5_DUNSA
YWFC_BACSU
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CHER_SALTY
HEMK_PASMU
SDC1_RAT
FBP2_STRPU
Y456_MYCGE
GUNA_RUMFL
BZTA_RHOCA
HRDC_STRCO
SCA3_MOUSE
5H5A_MOUSE
SH5A_MOUSE
NURG_LACLA
HUPN_BRAJA
IRK5_HUMAN
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Compugen Ltd.
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p08586 vaccinia vi
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084468 chlamydia t
1013474 kluyveromyc
p3639 bacilius su
p07014 escherichia
022608 dunaliella
p07864 escherichia
p07861 estalmonella
p07861 salmonella
p07862 prattus norv
p15216 strongyloce
p47694 mycoplasma
p16169 ruminococcu
052663 rhodobacter
p18184 streptomyce
035609 mus musculu
09cf92 lactococcus
045247 bradyrhizob
p48544 h g protein
p48545 m g protein
p48546 r g protein
                                                                                                                                                                                                    Q12913 homo sapien
Q29473 canis famil
Q64403 cavia porce
Q9u156 homo sapien
P04490 human adeno
P08586 vaccinia vi
P20539 vaccinia vi
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| PTA_HELPJ | HEMK_RICPR | ATPB_WHEAT | ATPB_HORVU | ATPB_AEGCO | AMYR_DROTE | E1BL_ADE07 | VL2_PAPVE | P3_HUMAN | PUR1_BACSU | AROA_MYCTU | AROA_MYCLE |
| Q9zku4 helicobacte | Q9zcb3 rickettsia | P20858 triticum ae | | aegilops | 076260 drosophila | ٠. | P11327 european el | P09131 homo sapien | P00497 bacillus su | P22487 mycobacteri | Q9cci3 mycobacteri |

ALIGNMENTS

| DR DR DR DR DR | 8888888 | 8888888888 | CC RT RA | RA RT | 2000 | | RESULT PTPJ_H ID P |
|--|--|---|---|---|---|--|---|
| EMBL; U10886; AAB36687.1; EMBL; D37781; BAA07035.1; HSSP; P18052; 1YFO. MIM; 600925; InterPro; IPR0033961; FN_III. InterPro; IPR000387; TYR_phosphatase. InterPro; IPR000387; TYR_prot_phphtase. Pfam; PF00041; fn3; 5. Pfam; PF00102; Y_phosphatase; 1. | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). | -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate! SUBCELIULAR LOCATION: Type I membrane protein!- PTM: N- AND O-GLYCOSYLATED!- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS!- DATABASE: NAME-PROW: NOTE-CD guide CD148 entry; -!- DATABASE: NAME-PROW: NOTE-CD guide CD148 entry; -!- WHW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm". | SEQUENCE FROM N.A. NEDLINE-95086212; PubMed-7994032; Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.; Molecular cloning, characterization, and chromosomal localization of a novel protein-tyrosine phosphatase, HPTP eta."; Blood 84:4186-4194(1994). -1- FUNCTION: MAY CONTRIBUTE TO THE MECHANISM OF CONTACT INHIBITION OF CELL GROWTH. | SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-95024024; PubMed-7937872; Gestman A., Yang Q., Tonks N.K.; "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced with increasing cell density."; proc. Natl. Acad. Sci. U.S.A. 91:9880-9884(1994). | Homo sapiens (Human). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9806; | 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta) (HPTP eta) (Density enhanced phosphatase-1) (DEP-1) (CD148 antigen). | LT 1 _HUMAN STANDARD; PRT; 1337 AA. D19013: D19085. |

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RESULT 2
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AC Q29473
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Matches 8
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Q29473; 002859;
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SMART; SM00060;
SMART; SM00194;
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
Signal; Glycoprotein; Transmembrane; Repeat;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTEN
N-LINKED (GLCNAC. . . .)
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Pred. No.
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0.068;
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TYPE-III 1.
TYPE-III 2.
TYPE-III 3.
TYPE-III 4.
TYPE-III 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Liver;
TISSUE-Liver;
MEDLINE-95305574; PubMed=7786018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sakamoto K., Kirita S., Baba T., Nakamura Takanaka A., Matsubara T.;
"A new cytochrome P450 form belonging to microsomes: purification, cDNA cloning, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; MCBI_TaxID=9615;
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Canis familiaris (Dog).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arch. Biochem. Biophys. 357:27-36(1998).
-!- FUNCTION: HIGH ACTIVITY FOR THE HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression system.
J. Biochem. 123:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tasaki T., Nakamura A., Itoh S., Ohashi K., Yamamoto Y., Iwata H., Kazusaka A., Kamataki T., Fujita S.; "Expression and characterization of dog CYP2D15 using bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last annotation update) Cytochrome P450 2D15 (EC 1.14.14.1) (CYPIID15) (P450 DUT2).
                                                                                                                                                         Oxidoreductase; Monooxygenase; El
Microsome; Endoplasmic reticulum.
                                                                                                                                                                                     Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450;
                                                                                                                                                                                                          MBL; AB004268; BAA2035/.1, ...
MSEP; P00179; IDT6.
InterPro; IPR001128; Cyt_P450.
PRONDERS: P450; 1.
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MEDLINE=98389575; PubMed=9721180;
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                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Expression and characterization of canine cytochrome P450 2D15.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98162950; PubMed=9504424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BEAGLE;
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381
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SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

TISSUE SPECIFICITY: LIVER. ALSO DETECTED IN SEVERAL OTHER TISSUES.

SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                SRDTEV
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                                                    Mismatches
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome P450 2D16 (EC 1.14.14.1) (CYPIID16).
CYP2D16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jiang Q., Voigt J.M., Colby H.D.;
"Molecular cloning and sequencing of a guinea pig cytochrome (CYP2D16): high level expression in adrenal microsomes.";
Biochem. Biophys. Res. Commun. 209:1149-1156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN=13; TISSUE=Adrenal cortex; MEDLINE=95251703; PubMed=7733969;
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Eukaryota; Metazoa; Chordata;
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382
                                       Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE ADRENAL CORTEX. SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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CATALYTIC ACTIVITY: H + reduced flavoprotein + oxidized flavoprotein + H(2)0.

SUBCELLULAR LOCATION: Membrane-bound. Endoplasmi TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN
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SRDTEV
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100.0%;
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                                                                              Score 6; DB 1
Pred. No. 5.4
0; Mismatches
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HEME (BY SIMILARITY).
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Human adenovirus type 7.

Viruses; dsDNA viruses, n
            EMBL;
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Q9UI56;
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                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
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Dijkema R., Dekker B.M.M., van Or
"Gene organization of the transfo
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                          use by non-profit institutions as long modified and this statement is not removed.
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P.20539;

0.1-FEB-1991 (Rel. 17, Created)

1.01-FEB-1991 (Rel. 17, Last sequence update)

T. 01-FCT-2001 (Rel. 40, Last annotation update)

7. 16-OCT-2001 (Rel. 40, Last annotation update)
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P08586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-87036903; PubMed=3021979;
Rosel J.L., Earl P.L., Weir J.P., Moss B.;
"Conserved TAAATG sequence at the transcriptional and translational initiation sites of vaccinia virus late genes deduced by structural and functional analysis of the HindIII H genome fragment.";
J. Virol. 60:436-449(1986).
  NCBI_TaxID=10249;
              Orthopoxvirus.
                                                                                                                                                                                                                                                                                    Late protein.
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SEQUENCE 88
                        Viruses; dsDNA viruses,
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01-MAY-1991 (Rel. 18, Created)
15-JUL-1998 (Rel. 36, Last sequing the control of the con
                                        PIR;
PDB;
                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS), MITCHELD T., Ernst S.R., Hackert M.L. "X-ray structure determination of a dimarenicola.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caudina arenicola (Sea cucumber) (Molpadia arenicola).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozo
Holothuroidea; Apodacea; Molpadiida; Caudinidae; Caudina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Globin D,
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"The complete DNA sequence of vaccinia Virology 179:247-266(1990).
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SEQUENCE FROM N.A.
MEDLINE=91021027; PubMed=2219722;
MEDLINE=91051027; PubMed=2219722;
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91265540; PubMed=2049384; Mauri F., Omnaas J., Davidson L., Whitfill C., Panino acid sequence of a globin from the sea (Molpadia) arenicola.";
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                      PIR; S15979; S15979.
PDB; 1HLM; 07-FEB-95.
InterPro; IPR000971;
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Paoletti E.;
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                                                                                                              HEMOGLOBIN CHAINS LABELED SIMILARITY: STRONG, TO C.P
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Matches
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ERRATUM.
MEDLINE=94040790; PubMed=8224889;
GU Z.-M., Martindale D.W., Lee B.H.;
Gu E.-I., Martindale D.W., Lee B.H.;
Gene 133:147-147(1993).
-i- CATALYTIC ACTIVITY: 5-phospho-beta-D-ribosylamine + diphosphate
-i- CATALYTIC ACTIVITY: 5-phospho-alpha-D-ribose 1-diphospha
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P35853;
01-JUN-1994
01-FEB-1996
InterPro; IPR000583; GATASE_2.
InterPro; IPR002375; Pur_pyr_pr_transf.
Pfam; PF00310; GATASE_2; 1.
PROSITE; PS00103; PUR_PYR_PR_TRANSFER; PARTIAL.
PROSITE; PS00443; GATASE_TYPE_II; 1.
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Gene 119:123-126(1992).
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Gu Z.-M., Martindale D.W., Lee B.H.;
"Isolation and complete sequence of t
synthase II in Lactobacillus casei.";
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15-DEC-1998
16-OCT-2001
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"Phylogenetic analysis of segment 10 from African horses
and cognate genes from other orbiviruses.";
Virus Res. 33:157-165(1994).
-1- FUNCTION: MAY PLAY A ROLE IN THE RELEASE OF VIRIONS
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SEQUENCE
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PROPEP 1 11
BY SIMILARITY
BY SIMILARITY
CHAIN 12 >194
AMIDOPHOSPHORIBOSYLTRANSFERASE.
ACT_SITE 12 12 GATASE (INVOLVED IN SUBSTRATE B
ACT_SITE 12 (CATALYSIS) (BY SIMILARITY).
                                                                                                                                                                                                 InterPro; IPR002565; Orbi_NS3. 1. 
Pfam; PF01616; Orbi_NS3; 1. 
ProDom; PD003183; Orbi_NS3; 1.
                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                           Nonstructural protein.
CHAIN 1 217
CHAIN 12 217
CHAIN 12 23663
                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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ISPD_CHLTR O84468;

STANDARD;

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RESULT 12
PYRE_KLULA
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Best Local S
Matches 5
                 Bai X., La
Submitted
                                                                                                                                                        PYRE_KLULA STANDARD; PRT; 226 AA (0.13474; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation updat (protate phosphoribosyltransferase (EC 2.4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                  Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.
-i- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis. Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytidylyltransferase) (MCT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
01-MAR-2002 (Rel.
                                              STRAIN-CBS 683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 282:754-759(1998).
-I- FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-D/UW-3/CX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=813;
                                                            SEQUENCE FROM N.A.
                                                                                      NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01295; ISPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of an obligate intracellular pathogen of humans:
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                   Larsen M., Meinhardt ed (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                         Similarity
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39,
                                                                                                      Saccharomycetaceae;
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                    EMBL/GenBank/DDBJ databases
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                                                                                                                   Saccharomycotina; Saccharomycetes
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2.4.2.10)
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(See http://www.isb-sib.ch/announce/
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RESULT 13
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                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                       Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Marescan E., Santana M., Schneider E., Schweizer J., Verapport G., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                     EMBL; X73124; CAA51637.1;
EMBL; Z99123; CAB15800.1;
PIR; S39736; S39736
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YWFC_BACSU
P39639;
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Pyrimidine biosynthesis; Transferase; Glycosyltransferase.

ACT_SITE 110 110 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ001358; CAA04694.1; HSSP; P08870; 1STO.
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                                                                                                                                                                                                  "Bacillus subtilis genome project: kb region from 325 degrees to 333 mol. Microbiol. 10:371-384(1993).
                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000836; Pribosyltran.
InterPro; IPR002375; Pur_pyr_pr_transf
Pfam; PF00156; Pribosyltran; 1.
                                                                                                                                                                                                                                                                                               MEDLINE=95020537; PubMed=7934828;
                                                                                                                                                                                                                                                                                                              STRAIN=168
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Orotidine 5'-phosphate + diphosphate + 5-phospho-alpha-D-ribose 1-diphosphate.

PATHWAY: FIFTH STEP IN PYRIMIDINE BIOSYNTHESIS.
SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
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protein in ROCC-PTA intergenic region.
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Hypothetical SEQUENCE 2

235 AA; 2

1; Complete 26839 MW;

proteome. 9A9A1608148D0FA6 CRC64

SubtiList; BG10627; ywfC

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RESULT
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Matches 5
Link A.J., Robison K., Church G.M.;
Link A.J., Robison K., Church G.M.;
Comparing the predicted and observed properties of proteins in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
-i- FUNCTION: TWO DISTINCT, MEMBRANE-BOUND, FAD-CONTAINING F RESPONSIBLE FOR THE CATALYSIS OF FUMARATE AND SUCCINATE THE THE CATALYSIS OF FUMARATE AND SUCCINATE THE FUMARATE REDUCTASE IS USED IN ANAEL
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"A 718-kb DNA sequence of the
corresponding to the 12.7-28.0
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Succinate dehydrogenase iron-sulfur protein (
                                                                                               MEDLINE=97443975; PubMed=9298646; Link A.J., Robison K., Church G.M.;
                                                                                                                            SEQUENCE OF 1-11.
STRAIN=K12 / EMG2;
                                                                                                                                                                 SEQUENCE OF 231-238 FROM N.A.
MEDLINE=84236108; PubMed=6376123;
Darlison M.G., Spencer M.E., Guest J.R.;
Darlison de sequence of the sucA gene encoding
"Nucleotide sequence of the sucA gene encoding
dehydrogenase of Escherichia coli K12.";
Lur. J. Blochem. 141:351-359(1984).
                                                                                                                                                                                                                                                                                                                   Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Mikī T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Dayis N.W., Kirkpatrick H.A., Goeden M.A., Rose E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
STRAIN-K12 / MG16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem.
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Bacteria; Proteobacteria;
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"Nucleotide sequence encoding the
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J. 223:507-517(1984).
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SEQUENCE FROM N...
KO J.H., Lee S.H
"A cDNA encodes
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InterPro; IPR001450; 4Fe4S_ferredoxin.
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PATHWAY: TRICARBOXYLIC ACID CYCLE.
SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING FOR FLAVOPROTEIN, AN IRON-SULFUR, CYTOCHROME B-556,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF 'PLANT-TYPE' 2FE-2S AND 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acceptor.
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Search completed: August 31, 2002, 12:23:58 Job time: 213 sec
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Interpro; IPR001149; Ribosomal_L18p.
Pfam; PF00861; Ribosomal_L18p; 1.
PRINTS; PR00058; RIBOSOMALL5.
ProDom; PD001394; Ribosomal_L18p; 1.
Ribosomal protein; rRNA-binding.
SEQUENCE 271 AA; 31218 MW; 482F53833D33B57E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal 5S RNA-binding protein from Dunaliella salina.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIBP FAMILY OF RIBOSOMAL PROTEINS.
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| hypothetical prote | protoporphyrinogen | hemK protein homol | protein-glutamate | protein-glutamate | response regulator | response regulator | protein-glutamate | hypothetical prote | probable ribosomal | succinate dehydrog | recombinase - Meth | succinate dehydrog | succinate dehydrog | succinate dehydrog | succinate dehydrog |

ALIGNMENTS

A; Experimental source: HeLa cells F; Yazaki, Y.; Hirai, H. F; Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H. Biood 84, 4186-4194, 1994 Blood 84, 4186-4194, 1994 A; Title: Molecular cloning, characterization, and chromosomal localization of a novel A; Title: Molecular cloning, characterization, and chromosomal localization of a novel A; Reference number: I52599; MUID:95086212 A; Accession: I52599 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: I-216, 'LTGVRKAA', 225-260, 'G', 262-285, 'GTEGGLDASNTERSRA', 302, 'S', 304, 'TAPV A; Cross-references: GB:037781; NID:9633072; PIDN:9AA07035.1; PID:9633073 C; Comment: Enhanced expression of this protein with increasing cell density suggests R;Ostman, A.; Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
A;Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, A;Reference number: I38670; MUID:95024024
A;Accession: I38670 A;Molecule type: mRNA A;Residues: 1-1337 <RES> A;Cross-references: EMBL:U10886; NID:g558754; PID:g558755 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human N;Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphata C;Species: Homo sapiens (man) RESULT I38670 F;1065-1287/Domain: protein-tyrosine-phosphatase homology cPTP>
F;72,82,93,104,142,172,192,231,258,278,342,351,376,391,396,413,431,501,525,536,582,60
F;1239/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1245/Binding site: substrate phosphate (Arg) #status predicted F:720-804/Domain: fibronectin type III 1 F:972-988/Domain: transmembrane #status F;1-35/Domain: signal sequence #status predicted <SIG>F;36-1337/Product: protein-tyrosine-phosphatase, recept F;118-197/Domain: fibronectin type III repeat homology A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine C;Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III re C;Keywords: glycoprotein; phosphorotein; phos F;539-617/Domain: F;284-356/Domain: F;365-445/Domain: F;453-530/Domain: F; 206-283/Domain: C; Function: A; Cross-references: GDB:385040; A: Map position: 19q13.4-19q13.4 A; Gene: GDB: PTPRJ C; Genetics: C; Accession: I38670; C;Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 22-Jun-1999 nct: protein tyrosine-phosphatase, receptor type J
nn: fibronectin type III repeat homology <3FNA>
nn: fibronectin type III repeat homology <3FNB>
nn: fibronectin type III repeat homology #status at
nn: fibronectin type III repeat homology <3FND>
nn: fibronectin type III repeat homology <3FND>
nn: fibronectin type III repeat homology <3FNB>
nn: fibronectin type III repeat homology <3FNF>
nn: transmembrane #status predicted <7MN> 152599 OMIM:600925 atypical <3FNC> ч #status predicted is enhanc ş

Query Match Best Local Similarity

100.0%;

Score 8; Pred. No.

DB 1; 0.19;

Length 1337;

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N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C;Accession: JC4157; S65962; S65898
R;Jiang, Q:; Voigt, J.M.; Colby, H.D.
Blochem. Biophys. Res. Commun. 209, 1149-1156, 1995
A;Title: Molecular cloning and sequencing of a guinea pig cytoch. A;Reference number: JC4153; MUID:95251703
A;Accession: JC4157
                                                                                                                                                           R:Jiang, Q.; Voigt, J.M.; Colby, H.D. Biochem. Biophys. Res. Commun. 209, 1149-187:Title: Molecular cloning and sequencing A; Reference number: JC4153; MUID:95251703 A; Accession: JC4153
                                                                                                                                                                                                                                                            cytochrome P450 2D16, CYP2D16 - guinea pig
N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Cavia porcellus (guinea pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000
C;Accession: JC4153; PC4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:U21486; NID:g862481
R;Sakamoto, K.; Kirita, S.; Baba, T.; Nakamura
Arch. Biochem. Blophys. 319, 372-382, 1995
A;Title: A new cytochrome p450 form belonging
A;Reference number: S65898; MUID:95305574
        0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homolog c; Keywords: adrenal gland; chromoprotein; endoplasmic reticulum; hem F; 305-468) Domain: cytochrome P450 homology <P45> F; 446/Binding site: heme iron (Cys) (axial ligand) #status predicted
                        A; Residues: 1-37
C; Comment: This
                                             A; Molecule type: protein A; Residues: 1-37 <JI2>
                                                                                 A;Cross-references: GB:U21486;
A;Accession: PC4052
                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-500 <JIA>
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C; Comment: This protein is a member of the CYP2D subfamily,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 2-37, 'X', 39
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A; Residues: 1-500 < SAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-500 < JIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytochrome P450 2D, endoplasmic reticulum - dog N;Alternate names: cytochrome P450 2D, microsomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:D17397; NID:g397824; PIDN:BAA04220.1; PID:g397825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
  Superfamily:
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Best Local
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les 6; Conserv
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                      protein is
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Conservative (
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    cytochrome P450
                                                                                                      NID: g862481; PIDN: AAA68479.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s; Score 6; DB 1; Pred. No. 15; 0; Mismatches
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of the CYP2D subfamily, 0 CYP2D6; cytochrome P450
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reticulum; heme;
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        RESULT
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QSRDT

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R:Hashimoto, K.; Nakanishi, T.; Kurosawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 89, 2209-2212, 1992
A;Title: Identification of a shark sequence resembling
A;Reference number: A41975; MUID:92196087
A;Accession: A41975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      major histocompatibility complex class I alpha 3 domain homolog - shark (Tr C;Species: Triakis scyllium C;Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 26-Aug-1999 C;Accession: A41975
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A41975
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A;Title: Gene organization of the transformation of the transform
                                                                                                                                                                                                         A;Cross-references: GB:M85291; NID:g213922
A;Note: sequence extracted from NCBI backbone (NCBIN:88077, NCBIP:88079); this ORF
A;Note: the source is designated as Triakis scyllia
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C; Accession: A03811
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                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-93 <HAS>
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A; Residues: 1-88 <DIJ>
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143-156, 1982
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5; Conserv
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llarity 100.0%;
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%; Pred. No. 48;
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keratin type I (clone Jn7-4) - African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: Z8-Oct-1995 #sequence_revision 07-Feb-1997 #text_change 10-Dec-1999
C;Accession: S55691
R;Adati, N.; Ito, T.; Koga, C.; Kito, K.; Sakaki, Y.; Shiokawa, K.
Biochim. Biophys. Acta 1262, 43-51, 1995
A;Title: Differential display analysis of gene expression in developing embryos of Xenop A;Reference number: S55691
A;Molecule type: mRNA
A;Residues: 1-105 <ADA>
A;Residues: 1-105 <ADA>
A;Residues: 1-105 <ADA>
                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI backbone (NCBIP:115752) R;Jagura-Burdzy, G.; Khanim, F.; Smith, C.A.; Thomas, C.M. Nucleic Acids Res. 20, 3939-3944, 1992 A;Title: Crosstalk between plasmid vegetative replication and A;Reference number: S26289; MUID:92375675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: san protein; single-stranded DNA-binding protein Ssb C;Species: plasmid RK2 C;Species: plasmid RK2 C;Date: 18-Feb-1994 #sequence_revision 17-May-1996 #text_change 03-Dec-1999 C;Accession: S07258; A44020; S26289 R;Smith, C.A.; Thomas, C.M.
J. Mol. Biol. 175, 251-262, 1984 A;Reference number: S07258; MUID:84216332 A;Accession: S07258; MUID:84216332
                                                  Q
                                                                                                                                                                                        C;Superfamily: single-stranded DNA-binding protein; C;Keywords: single-stranded DNA binding F;19-95/Domain: single-stranded DNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-37 <LES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A44020; MUID:93015931
A; Contents: incompatibility group P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X00713; NID:g45775; PIDN:CAA25305.1; PID:g45776 A;Note: the authors translated the codon CAC for residue 64 as Gln R;Lessl, M.; Balzer, D.; Pansegrau, W.; Lanka, E. J. Biol. Chem. 267, 20471-20480, 1992
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                                                                                                                                                                                                                                                                         C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A44020
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A; Residues: 1-116 <SMI>
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Pred. No.
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                                                                                                          R, Johnson, G.r.
R, Johnson, G.r.
Submitted to GenBank, June
Submitted to GenBank, June
                                                                                                                                                                                                                                                                     RESULT 10
QQVZ28
A;Cross-references: GB:M35027; NID:g335317; C;Superfamily: vaccinia virus H8 protein C;Keywords: late protein
                                                                                                                                                                      H8 protein - vaccinia virus (strain N;Alternate names: H7R protein C;Species: vaccinia virus C;Date: 30-Sep-1992 #sequence_revisi C;Accession: G42514
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QQVZH8
                                                        A; Reference number: A33:
A; Accession: G42514
A; Molecule type: DNA
A; Residues: 1-146 < JOH>
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A; Residues: 1-118 <GRA>
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A;Reference number: A93022; MUID:87036903
A;Accession: H24481
A;Molecule type: DNA
A;Residues: 1-129 <ROS>
A;Cross references: GB:M13209; NID:g335739;
C;Superfamily: vaccinia virus H8 protein
C;Keywords: late protein
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A;Accession: T17967
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Rosel, J.L.; Earl, P.L.; Weir, J.P.; Moss, J. Virol. 60, 436-449, 1986
A;Title: Conserved TAAATG sequence at the tr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H8 protein - vaccinia virus (strain WR) (fragment) C;Species: vaccinia virus C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988
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A;Experimental source: specific host Chlorella strain NC64
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C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                  #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
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62;
PIDN:AAA48094.1; PID:g335442
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probable 17K protein - vaccinia virus (strain Ankara)
C:Species: vaccinia virus
A:Variety: Strain Ankara
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T37373
R:Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain Reference number: Z20877
A:Accession: T37373
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 1-146 <ANTY
A:Cross-references: EMBL:U94848; PIDN:AAB96510.1
A:Experimental source: strain Ankara
C:Genetics:
A:Note: MVA097R
C:Superfamily: vaccinia virus H8 protein
                                                                                                                                                                                                                                                                                                                                         dynein heavy chain 3 - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Species: O4-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 21-Jul-2000
C;Accession: $72241
R;Porter, M.E.; Knott, J.A.; Myster, S.H.; Farlow, S.J.
Genetics 144, 569-585, 1996
A;Title: The dynein gene family in Chlamydomonas reinhardtii.
A;Reference number: $72239; MUID:97044450
A;Accession: $72241
A;Status: preliminary; nucleic acid sequence not shown
A;Status: preliminary; nucleic acid sequence not shown
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S72241
                hypothetical protein all3520 [imported] - Anabaena C;Species: Anabaena sp.
                                                  AI2245
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A;Introns:
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A; Residues: 1-147 < POR>
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                                                                                                                     DTEVL 103
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                                                                                                                                                                                                                                                                   44/1; 109/3
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5; Conserv
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Pred. No.
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Pred. No.
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                                     7120)
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GB:AP001519;

GB:BA000004; NID:g10176109; PIDN:BAB07305.1;

GSPDB:G

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C;Species: Caudina arenicola
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 19-May-2000
C;Accession: S15979
R;Maur1, F:; Omnaas, J:; Davidson, L.; Whitfill, C.; Kitto, G.B.
Blochim. Blophys. Acta 1078, 63-67, 1991
A;Title: Amino acid sequence of a globin from the sea cucumber Caudina (Molphyseference number: S15979; MUID:91265540
A;Accession: S15979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: globin; globin homology
C;Keywords: blocked amino end; blood; chromoprotein; dimer; erythrocyte; heme; iron;
E;12-157/Domain: globin homology <GLB>
E;1/Modified site: blocked amino end (Gly) (probably acetylated) #status experimental
E;73/Binding site: oxygen (His) (distal axial ligand) #status predicted
E;704/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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A; Molecule type: DNA
A; Residues: 1-166 <S
A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                    acetyltransferase BH3586 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                               A;Reference number: A83650;
A;Accession: B84098
                                                                                                                                                                                  R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B84098
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A; Residues: 1-158 <BIO>
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A;Experimental source: strain PCC 7120
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A; Residues: 1-154 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic
                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                 C; Accession: B84098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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Best Local S
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5; Conserv
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                                      <STO>
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100.0%;
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78;
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; Yasuda, M.; Tabata
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                                                                                                                                                                                                                                                                                                      F.; H
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| Db 2 SEATCH completed: August 31, 2002, 12:20:42 Job time: 122 see | A;Experimental source: strain C-125 C;Genetics; A;Gene: BH3586 A;Gene: BH3586 Query Match Best Local Similarity 100.0%; Pred. No. 83; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 2 SRDTE 6 Qy 2 SRDTE 6 |
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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                      Score
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length: 2000000000
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3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
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16: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                Sequence #1 for ep hubEP-1. Homo sap Drosophila melanog T cell antigen rec Lipopolysaccharide Peptide Q0130 used Peptide R0130 used Maize Dof peptide ERA binding domain
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Propionibacterium Human protein SEQ
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| ABG08331 | BB64520 | AG82613 | AG54774 | AU01781 | AG32239 | AG32240 | AY94451 | ABB69076 | AG72257 | AAW55386 | AW98427 | AY37759 | AB80153 | AU30554 | AW55524 | AAY69981 | AB25184 | BG16051 | AAB57124 | BG18304 | AG01891 | AU53773 | AU39232 | AY50927 | 651 | 640 | 35 | 733 | 36 | AAB03842 | 84 | AAR25119 | AAM39020 |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | rosophila melan | ᅀ. | dopsis | rete | S | sqob | Human inflammation | വ | actor | H. pylori ORF 11ge | H. pylori GHPO 398 | Amino acid sequenc | bacterium o | el human secre | lori ORF 29e | N-ace | lyptus o | human di | prosta | human dia | Human secreted pro | Propionibacterium | onibact | etal bra | 2 | hone | Human brain expres | Propionibacterium | onibacterium | in fragment | ein fragm | Non-B Hen | Human polypeptide |

ALIGNMENTS

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AAU03200 standard; peptide; 8

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XX WO Novel antibody for modulating angiogenesis and endothelial cell migration and proliferation, binds endothelial cell receptor ty phosphatase/density enhanced phosphatase-1 -ECRTP/DEP-1; endothelial cell receptor tyrosine phosphatase; density enhanced phosphatase-1; anti-inflammatory; antipsoriatic; antiheumatic; antidiabetic; antiatherosclerotic; cytostatic; osteopathic; angiogenesis inhibitor; tumour; cancer. WPI; 2001-570681/64. 01-MAR-2000; 2000US-0516728 27-FEB-2001; 2001WO-US06178 07-SEP-2001. Mammalia. (UYVA-) UNIV VANDERBILT. WO200164750-A2 Sequence #1 for epitope of ECRTP/DEP-1 ectodomain binding antibody. 03-JAN-2002 то, Takahashi T, (first entry) Mernaugh

receptor tyrosine

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AAR85203
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and may be an ECRTP/DEP-1 modulator, ECRTP/DEP-1 dimerisation promoter or antagonist and angiogenesis inhibitor. The purified antibody blocks endothelial migration and proliferation and inhibits angiogenesis in disorders such as inflammatory disorders including immune and non-immune inflammation, chronic articular rheumatism and psoriasis, disorders associated with inappropriate invasion of vessels such as diabetic retinopathy, neovascular glaucoma, capillary proliferation in atheresclerotic plaques, osteoporosis and cancer associated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a novel purified antibody (or its fragment or derivative) which preferentially binds an endothelial cell receptor tyrosine phosphatase/density enhanced phosphatase-1 (ECRPP/DEP-1). The antibody has antiinflammatory, antipsoriatic, antirheumatic, antidiabetic, antiatherosclerotic, cytostatic and osteopathic activities antidiabetic, antiatherosclerotic, cytostatic and osteopathic activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         such as solid tumours, solid tumour metastases, angiofibromas, retrolental fibroplasia, hemangiomas, Kaposi's sarcoma and similar cancers. This sequence is peptide sequence #1 for epitope ECRTP/DEP-1 ectodomain binding antibody used to modulate angiogenesis, described: the method of the invention.

Note: This sequence for ECRTP/DEP-1 epitope, given in example 4, different that given in claim 3 (AAU08802).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 82;
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A cDNA clone was obtd.
                              Claim 4; Page 34-38; 51pp; English.
                                                                                                                          WPI; 1995-393079/50.
N-PSDB; AAT06027.
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                                                                                                                                                                                                                                    03-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                           New density enhanced protein tyrosine phosphatase - used to develop prods. to modify transcription, translation and/or activity of
                                                                                                                                                                                                                                                                                                                                                                                        huDEP-1
                                                             tyrosine phosphatase(s).
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(see AAT06027) from
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The sequence data for this patent did not form specification, but was obtained in electronic f

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ABB57737-ABB72072)

at ftp.wipo.int/pub/published_pct_sequences

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Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that encoded a novel density-enhanced Type III receptor-like PTP, designated huDEP-1 (AAR85203). huDEP-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for prevention of abnormal or malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell:cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical.
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                                                                                                                                                                  Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                           Venter JC,
                                                                                                                                                                                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001;
                                                                                                                                                                                                     New isolated nucleic a
genes from Drosophila
                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY
                                                                                                                                                                                          interactions -
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DB; ABL05141.
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2000US-0614150.
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100.0%; Pr
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Best Local
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        Lipopolysaccharide
                                                           24-MAY-1994
                                                                                                              AAR51956;
                                                                                                                                                              AAR51956 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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14-OCT-1998;
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98JP-0328761.
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protein (peptide fragment).
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Matches 5
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                                                                                                                                                                                                       JP2000135087-A.
                                                                                                                                                                                                                                                                                                      Serum type identify; t
                                                     29-OCT-1998;
                                                                                                    29-OCT-1998;
                                                                                                                                                       16-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                              Peptide Q0130 used in TT virus antibody determination.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB03843 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptide induced in macrophage(s) by useful e.g. as antitumour, antiinflammatory agent, also related nucleic acid, antibodies
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                                                                                                                                                                                                                                                         TT virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 67; 108pp; English
                                                                                                                                                                                                                                                                                                         classification; TT virus; antibody; viral infection; treatment.
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3. 26;
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A method for serum type classification of TT virus (also known as hepatitis TT virus) has been identified. The method relies on the use of peptide fragments of the virus. The invention also relates to the use of TT virus peptides for anti-TT virus antibody determination. The anti-TT virus antibodies and the serum type classification method, can be used to screen TT virus, to determine its route of infection, and seroconversion. The classification of TT virus may lead to improved treatment of viral disease. The present sequence represents a fragment of TT virus protein used in the course of the invention.
                                         A method for serum type classification of TT virus (also known as hepatitis TT virus) has been identified. The method relies on the use of peptide fragments of the virus. The invention also relates to the use of TT virus peptides for anti-TT virus antibody determination. The anti-TT virus antibodies and the serum type classification method, can be used to screen TT virus, to determine its route of infection, and seroconversion. The classification of TT virus may lead to improved treatment of viral disease. The present sequence represents a fragment of TT virus protein
                                                                                                                                                                                 Claim
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Sequence
                                used
                                                                                                                                                                                                            Peptides for determination of anti-TT virus antibody and method serum classification of TT virus using the peptides
                                                                                                                                                                                                                                                         WPI; 2000-415430/36.
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                                course of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TT virus; antibody; viral infection;
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Best Local Similarity
Thehes 5; Conserve
                                                                               of maize are named zein) and 27-10 gamma-zein genes, so as to enhance gamma-zein production and lower alpha-zein production, so that methionine and lysine content of plant seed is increased over the content in native plant. PBF protein is a novel endosperm-specific cys2-cys2 zinc finger-type DNA binding protein of the DOF family. The transgenic monocot plant is a maize plant and expresses increased levels of methionine and/or lysine content in the seeds of the plant. The development of transgenic lines which supply higher levels of methionine reduces the need for methionine supplements for corn-soybean meal poultry feed and increased lysine content of either the cereal grains or the oilseed crops results in significant added nutritional value. The present is maize dof peptide domain ZMDOF2. This sequence contains a dof domain at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a transgenic monocot plant comprising an isolated DNA operably linked to a promoter, which is expressed to yield a prolamin box binding factor peptide (PBF). PBF then binds to promoter regions of 22-kD alpha-zein (prolamin seed storage proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel transgenic monocot plant, such as maize plant having increased methionine and/or lysine content in seeds, comprises recombinant prolamin box binding factor peptide gene
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sequence shown in sequence listing of the specif
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nutritional value; ZMDOF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to ERA binding domain polypeptides (AAG9955-AAG9989 and AAM00010-AAM0021). The era gene in Escherichia coli codes for an essential GTPase protein able to autophosphorylate at serine and/or threonine residues. The protein has potential antimicrobial and antibacterial activity and is useful in screening for antagonists, agonists and for compounds with antibiotic activity. The proteins are also useful in determining their role in pathogenesis of infection, dysfunction and disease and could be used as part of a vaccine and/or posture the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and/or particle the protein and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and could be used as part of a vaccine and a vaccine and a vaccine a
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  AAU54869;
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                                                 AAU54869 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide therapy.
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SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                   presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful vaccinating against and diagnosing infections, especially usefureating acne vulgaris -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAU39105-AAU68017 represent Propionibacterium acnes
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02-JUN-2000;
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27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                          The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopolesis regulating activity, tissue growth factor activity, hammatopolesis regulating activity, tissue growth factor activity, hammatopolesis, activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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Zhao
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N-PSDB; AAK51829.
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                                                                                                                                                                                                                                                                                                                                                                                                                            useful in diagnosis and gene therapy
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01-SEP-2000;
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Wang D,
Yang Y,
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2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663325.
2000US-0693325.
2000US-0728422.
                                                                                                                           Conservative
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Wang J, Zhang J, Ren F
             Protein;
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100.0%
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                                                                                                                         Score 5; DB 2; Pred. No. 91; 0; Mismatches
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and J, Ren F,
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91;
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62.5%; ilarity 100.0%; Conservative

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Mismatches

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Length 68

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assays IUL
C.N.S disorders.
Note: The sequen
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.
                                                                immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, cancer diagnosis and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                       Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
Sequence
                         specification.
                                                                                                                                                                                                                                                                                      Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200153312-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM39020;
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                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leukaemia.
                                                                                                                                                                                                                   invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic.
                                                                                                                                                                                                                                                                                                                                                                      YT,
QA,
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DB; AAI58176.
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Zhou P,
                                        sequence
68
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Wehrman T, X
Goodrich R,
                                         data
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system injuries •
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Xu C,
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Zhang J;
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29-NOV-1990;
16-JAN-1991;
19-APR-1991;
07-JUN-1991;
                                                                                                                                                                                                                                                         This sequence is one of 12 claimed antigen sequences specific to NANBH virus. The antigens can be used singly or in combination in an ELISA diagnosis of hepatitis. See AAR24946 and AAR25110-R25121
        16-MAY-2000
                       JP2000135087-A
                                       TT virus
                                                              Serum type classification;
                                                                            Protein fragment #3 used in TT virus antibody determination
                                                                                              20-OCT-2000
                                                                                                              AAB03841;
                                                                                                                            AAB03841 standard; protein;
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                         Claim 1; Page 49;
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91JP-0232590.
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90JP-0325435
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100.0%; Pr
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96;
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                                                                                                 Peptides for determination of anti-TT virus antibody serum classification of TT virus using the peptides
                                                                                                                                                                                                                                                                                                        Serum type classification;
                                                                                                                                                                                                                                                                                                                                                                                                 AAB03842 standard; protein;
                                                                           Claim 3; Page
                                                                                                                                   WPI; 2000-415430/36
                                                                                                                                                                                29-OCT-1998;
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                                                                                                                                                                                                                                                                         TT virus
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                                                                                                                                                          (SRLS-) SRL KK
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                                                                                                                                                                                                                                                                                                treatment
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A method for serum type classification of TT virus (also known as hepatitis TT virus) has been identified. The method relies on the use of peptide fragments of the virus. The invention also relates to the use of TT virus peptides for anti-TT virus antibody determination. The anti-TT virus antibodies and the serum type classification method, can be used to screen TT virus, to determine its route of infection, and seroconversion.

thod, can be used to and seroconversion.

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Query Match 62.5%; Score 5; DB 21; Le Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0;

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Sequence 90 AA;

The classification of TT virus may lead to improved treatment of viral disease. The present sequence represents a fragment of TT virus protein used in the course of the invention.

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| 212 | 209 | 206 | 205 | 201 | 192 | 192 | 192 | 188 | 187 | 183 | 180 | 180 | 178 | 178 | 178 | 171 | 166 | 160 | 147 | 146 | 146 | 146 | 143 | 143 | 119 | 118 | 116 | 113 |
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| Q9S239 | Q18970 | Q96GV9 | 072628 | Q94148 | Q9J7M1 | Q9J7M2 | Q9BSU2 | Q9DB82 | Q9RXH1 | Q985S5 | Q9ZKK0 | Q9J7L8 | Q9D7H8 | Q9Y6D2 | Q9H0Y4 | Q91881 | Q9K6Y8 | Q9NQH6 | Q96390 | Q9JFA9 | 057208 | Q9K527 | Q9D6A6 | Q9H5V1 | 085651 | Q98515 | Q02327 | Q9D5W2 |
| Q9s239 streptomyce | Q18970 caenorhabdi | Q96gv9 homo sapien | 072628 human immun | Q94148 caenorhabdi | Q9j7ml tt virus. o | tt v | Q9bsu2 homo sapien | Q9db82 mus musculu | Q9rxh1 deinococcus | Q985s5 rhizobium l | Q9zkk0 helicobacte | Q9j718 tt virus. o | mus | homo | $\overline{}$ | Q9i881 gallus gall | | | Q96390 chlamydomon | | O57208 vaccinia vi | Q9k527 mycobacteri | Q9d6a6 mus musculu | Q9h5v1 homo sapien | Ø | Q98515 paramecium | Q02327 enterobacte | Q9d5w2 mus musculu |

ALIGNMENTS

| Оу | Qu Ве | SQ | Κ. R | ᄝ | DR | R R | RT 3 | RA A | R R | RF 3 | R.P | R OX | 8 | 8 8 | B | ם ה | 33 | AC E | Q9NPR5 | RESULT |
|--|--|---|-------------------------|-------|--------------------|---|---|---------|---------------------------|--|----------|------------------|--------------------------------------|--|--------------|---|----------------------|------|---------------------------------------|--------|
| 1 QSRDTEVL 8 324 QSRDTEVL 331 | Query Match 100.0%; Score 8; DB 4; Length 425; Best Local Similarity 100.0%; Pred. No. 0.12; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps | NON_TER 425 425 SEQUENCE 425 AA; 45078 MW; BD1ACA5D345B7027 CRC64; | SMART; SM00060; FN3; 2. | 5961; | 59057; CAB94390.1; | human gene transcripts."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. | "The European IMAGE consortium for integrated Molecular analysis of | | [2] SEQUENCE FROM N.A. | Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. | ROM N.A. | NCBI_TaxID=9606; | ia; Primates; Catarrhini; Hominidae; | Homo sapiens (Human). Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; | NE PHOSPHATA | 01-JUN-2001 (Trembirel, 17, Last sequence update) | 2000 (TrEMBLrel. 15, | | R5 OQNDRS DRFITMTNARY: DRT: 425 AA | E7 1 |

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Q15255;
Q1-NOV-1996
Q1-NOV-1996
  STRAIN=C57BL/6J; TISSUE=EMBRYO;
MEDLINE=2108560; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.
                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
2610016F07RIK PROTEIN.
POV1 OR 2610016F07RIK.
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Pfam; PF00102; Y_phosphatase;
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00060; FN3; 6.
SMART; SM00194; PTPC; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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SIGNAL
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PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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Mammalia; Eutheria;
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MBL, D37791; BAA07035.1; -.
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Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Blake J., Buft C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Streptomyces coelicolor.
Bacteria; Firmicutes; Ac
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01-OCT-2000 (TrEMBLrel.
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PUTATIVE THIOL-SPECIFIC
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a
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Bentley S.D.,
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EMBL; AK011417; BAB27605.1; -.
MGD; MGI:1931352; Pov1.
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01-JUN-2001
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STRAIN=CV. COLUMBIA;

MEDLINE-21016719; Pubmed=11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
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F14G24.25.
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Lagos R., Baeza M., Corsini v.,
Castillo J.A., Vergara C., Monasterio O
Castructure, organization and characteri
"Structure, organization of microcin
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EMBL; AF063590; AAL08403.1; -.
SEQUENCE 524 AA; 59120 MW; 2F
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MEDLINE=21537172; PubMed=11679081;
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Bacteria; Proteobacteria;
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Bacteriol. 181:212-217(1999).
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Arch. Virol. 145:1385-1398(2000).

EMBL; AB030487; BAA90406.1; -.

InterPro; IPR004219; TT_ORF1.

Pfam; PF02956; TT_ORF1; 1.

SEOUENCE 765 AA; 90225 MW; E84
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01-OCT-2000
01-DEC-2001
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TT virus.
                   Viruses; ssDNA vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka Y., Orito E., Ohno T., Nakano T., Hayash
Mukaide M., Iida S., Mizokami M.;
"Identification of a 23kDa protein encoded by p
frame 2 of TT virus (TTV) genotype 1 different
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NCBI_TaxID=68887;
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InterPro; IPR002917; MMR_HSR1.
Pfam; PF01926; MMR_HSR1; 1.
PRINTS; PR00326; GTP10BG.
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EMBL; AC019018; AAG52287.1;
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Mus musculus (Mouse).
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Metazoa; Rodentia;
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O9QXG1;
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O1-MAY-2000 (TrEMBLrel. 13, Last seq)
O1-JUN-2001 (TrEMBLrel. 17, Last ann)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-20417334; PubMed-10963344;
Tanaka Y., Orito E., Ohno T., Nakan
Mukaide M., Iida S., Mizokami M.;
"Identification of a 23kba protein
frame 2 of TT virus (TTV) genotype
       Bartman A.E.,
                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genotypes."
                                                             NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genotypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanaka Y., Orito E., Ohno T., Nakar
Mukaide M., Iida S., Mizokami M.;
"Identification of a 23kDa protein
frame 2 of TT virus (TTV) genotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20417334; PubMed=10963344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JGS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=68887;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663
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                                                                                                                                                                                                                                                                                                                                         663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB030489; BAA90412.1; -
Pro; IPR004219; TT_ORF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB030488; BAA90409.1; -
Pro; IPR004219; TT_ORF1.
PF02956; TT_ORF1; 1.
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     N.A.
Shekels
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90401 MW;
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b; Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Score 6; DB 1; pred. No. 38; 0; Mismatches
                                                                                                                                                             Last sequence update)
Last annotation updat
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Last sequence update)
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     Anway
                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
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       Z
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5.38;
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   Gipson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi K., Kato T.,
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     Moccia
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RA Ballew R.M. Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Ferrar C., Ferriera S., Fleischmann W.,
RA Cholek A., Gong F., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., J.H., Guz., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibegvam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Lang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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SMART; SM00181; EGF; 1.
SMART; SM00001; EGF; 1ike; 2.
SMART; SM00539; NIDO; 1.
SMART; SM00216; VWD; 1.
SMART; SM00216; VWD; 1.
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Best Local
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O9W4M7: O97423; O97424;
01-MAY-2000 (TrEMBLrel. 1:
01-MAY-2000 (TrEMBLrel. 1:
01-OCT-2001 (TrEMBLrel. 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG4857 OR EG:EG0007.4 OR
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"Identification and Structure of a Mouse
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EMBL; AF218265; AAF23
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InterPro; IPR003886; Nidogen_ext
InterPro; IPR001846; Vwd.
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13,
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(Fruit fly).
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Last annotation updat
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5. 62;
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Best Local S
Matches
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Best Local S
Matches 6
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Q9WUX1;
01-NOV-1999 (TrEMBLrel. 12, Cr
01-NOV-1999 (TrEMBLrel. 12, La
01-NOV-1999 (TrEMBLrel. 12, La
APOBEC-1 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              melanogaster.";
Science 287:2220-2222(2000).
EMBL; AE003430; AAF45924.1; -
EMBL; AL033125; CAA21827.1; AIT_SEQ.
EMBL; AL033125; CAA21828.1; AIT_SEQ.
EMBL; AL033125; CAA21828.1; AIT_SEQ.
E1yBase; FBqn0026083; CG4857.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wawang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu S., Zhu X., Zhu S., Zhu S.
                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98335789; Greeve J., Axelos
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
[1]
                                                                                                                                                      NON_TER
                                                                                                                                                                            EMBL;
                                                                                                                                                                                               Arterioscler.
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Hypothetical
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        Similarity
5; Conserv
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1911 AA;
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llarity 100.0%;
Conservative
          Conservative
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D., Welker S.,
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62.5%; su
100.0%; Pr
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Last annotation update)
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                            Score 5;
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      red. No. 18;
Mismatches
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Smith H.O.,
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Best Local S
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Matches 5
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O917U4;
01-DBC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
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Q917U3;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORF1
                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TT virus.
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TT virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=68887;
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"Transfusion transmitted virus
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virus (TTV)
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PRELIMINARY;

PRT;

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Search completed: August 31, 2002, 12:23:05 Job time: 215 sec
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                                                                                                                          Query Match 62.5%; Score 5; DB 10; Length 101; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                          Ohta N.;

Ohta N.;

J. Plant Res. 110:235-245(1997).

EMBL; D63676; BAA22827.1; -.

HSSP; P00274; 1T7P.

InterPro; IPR000063; Thiored.
Pfam; PF00085; thiored; 1.

PRINTS; PR00421; THIOREDOXIN.
PROSITE; PS00194; THIOREDOXIN; 1.

Redox-active center.

Redox-active center.

Redox-active center.
                                                                                                                                                                                                                                                                                                                                                                     O22031;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
THIOREDOXIN M.
TRXM.
Cyanidium caldarium.
Cyanidium.
Charyota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
Cyanidium.
NCBL_TaxID-2771;
[1]
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=RK-1;
                                                                     4 DTEVL 8
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Minimum DB
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Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                        Score
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSRDTEVL 8
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                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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| 40 | n 4 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 |
|--------------------|----------|-------------|----------|--------------------|--------------------|--------------------|--------------------|-------------------|----------|----------|--------------------|----------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|----------|----------|----------|----------|--------------------|----------|--------------------|----------|-------------------|----------|-----|----------|----------------|--------------|----------|--------------------|
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| /3./ | ، د | u | ω | · | · | ω | ω | 73.7 | · | w • | 73.7 | · | ω. | ω. | ω | ω | ω | ω | 9 | 6 | 6. | 6. | 6. | <u>ه</u> | σ. | 8 | 8 | 78.9 | 8 | 8 | 8 | 8 | 78.9 | 78.9 |
| 440 | | 287 | 255 | 183 | 168 | 165 | 162 | 134 | 109 | 109 | 109 | 109 | 109 | 109 | 109 | 109 | 75 | 75 | 2443 | 1872 | 1042 | 1042 | 1033 | 361 | 234 | 1911 | 525 | 513 | 513 | 513 | 431 | 422 | 395 | 385 |
| 7 | 3 6 | ၁ ၁ | 21 | 21 | 22 | 21 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 18 | 22 | 22 | 22 | 22 | 22 | 22 | 19 | 22 | 22 | 22 | 22 | 22 | 22 | 21 | 21 | 21 |
| AAB12384 | 33712501 | AACROK13 | AAG40091 | AAG40092 | AAU29724 | AAG40093 | ABG11474 | AAO05568 | AAM01619 | AAM26283 | AAM13876 | AAM66007 | AAM53628 | ABB18303 | ABB32821 | ABB27651 | AAB68241 | AAW26420 | ABB60521 | AAM79160 | AAY97699 | AAU37752 | AAM01097 | ABB68291 | AAW61015 | ABB61038 | AAM42068 | AAB68510 | 19 | AAM40282 | AAM42384 | AAG54588 | AAG54589 | AAG54590 |
| Naphthatene dioxyg | - | enidermidis | | Arabidopsis thalia | Novel human secret | Arabidopsis thalia | Novel human diagno | Human polypeptide | | | Peptide #310 encod | | Human brain expres | #302 | Peptide #327 encod | Human peptide #302 | Protein encoded by | Swinepox virus Hin | | | | () | CFE 100 protein se | | Streptococcus pneu | ō | Human polypeptide | | | | an polypeptide | mays protein | mays | Zea mays protein f |

ALIGNMENTS

Sequence #1 for epitope of ECRTP/DEP-1 ectodomain binding antibody.

03-JAN-2002

(first entry)

AAU03200;

AAU03200 RESULT

ب

AAU03200 standard; peptide;

8 A

Novel antibody for modulating angiogenesis and endothelial cell migration and proliferation, binds endothelial cell receptor tyrosine phosphatase/density enhanced phosphatase-1 07-SEP-2001 ECRTP/DEP-1; endothelial cell receptor tyrosine phosphatase; density enhanced phosphatase-1; anti-inflammatory; antipsoriatic; antirheumatic; antidiabetic; antiatherosclerotic; cytostatic; WPI; 2001-570681/64. 01-MAR-2000; 2000US-0516728 Daniel TO, (UYVA-) UNIV VANDERBILT. 27-FEB-2001; 2001WO-US06178 WO200164750-A2 Mammalia. osteopathic; Takahashi T, angiogenesis inhibitor; tumour; cancer Mernaugh R;

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RESULT
AAR85203
ID AAR8
XX AAR8
XX AAR8
AC AAR8
XX Dens
KW Dens
KW huDE
XX Homc
XX HOMC
PN WO95
XX O9-N
XX O9-
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Matches 8; Conser
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   A cDNA clone was obtd.
                                                                      Claim 4; Page 34-38; 51pp; English
                                                                                                                                                                              New density enhanced protein tyrosine phosphatase - used to develop prods to modify transcription, translation and/or activity of
                                                                                                                                                                                                                                                                                              WPI; 1995-393079/50.
N-PSDB; AAT06027.
                                                                                                                                                                                                                                                                                                                                                                                                      Oestman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1995;
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Note: This sequence for ECRTP/DEP-1 epitope, given in example 4, differs from that given in claim 3 (AAU08802).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a novel purified antibody (or its fragment or derivative) which preferentially binds an endothelial cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COLD-) COLD SPRING HARBOR LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Density enhanced
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); Mismatches
       from
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                                                      WPI; 2000-500381/45.
N-PSDB; AAC01897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    that encoded a novel density-enhanced Type III receptor-like PTP, designated hubEp-1 (AAR85203). hubEp-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for prevention of abnormal or malignant cell growth.
Sequence
                  DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                           Claim 13;
                                                                                                                                                                             diagnostic,
                                                                                                                                                                                                                                                 Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                       06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG01891;
                                                ends and can therefore be used to obtain full length cDNAs and genomic
                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                  EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG01891 standard;
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                                                                                                                                                                                                                                                                                        26-FEB-1999;
                                                                                                                                                                                                                                                                                                           21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                       therapy;
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                                                                                                                                                           SEQ ID 5972;
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 121
                                                                                                                                                                             torensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag; secreted
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RESULT
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                   Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
Arabidopsis thaliana
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                                                            protein fragment SEQ ID NO: 46971.
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990S-0123180

990S-0123581

990S-0126784

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990S-0130497

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990S-0132485

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RESULT
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16-OCT-1999
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                                                                          Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                          06-SEP-2000.
                                          EP1033405-A2
                                                          Arabidopsis thaliana
                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 14283.
                                                                                                                                                AAG14425;
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         25-FEB-2000; 2000EP-0301439
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                                                                                                                                                                 Protein;
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                                                                                     pathway;
promoter;
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                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                   Arabidopsis thaliana
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75.0%;
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Pred. No. 1.2e+02;
2; Mismatches 0
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                                                                                                                                                                                                                                                                                                              fragment SEQ ID NO: 46970.
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19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

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                New isolated nucleic a
genes from Drosophila
interactions -
                                              WPI; 2001-656860/75.
N-PSDB; ABL08914.
                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
  Disclosure; SEQ ID NO 21225; 21pp + Sequence Listing; English
                                                                                                   23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                            Drosophila melanogaster polypeptide
                                                                     Venter JC,
                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                         27-SEP-2001.
                                                                                                                                                        WO200171042-A2
                                                                                                                                                                       Drosophila melanogaster
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                                                                                                                                                                                                                                           ABB64811;
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                                                                                    ) PE
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                                                                                    CORP NY.
                                                                     Adams M,
                                                                                                   2000US-191637P
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75.0%;
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                                                                     PWD,
                        detection reagent for detecting for elucidating cell signalling
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. 1.2e+02;
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                        1000 or more and cell-cell
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9908-0144332 9908-0144333 9908-0144333 9908-0144632 9908-014508 9908-014508 9908-014508 9908-014508 9908-014508 9908-014508 9908-014508 9908-014508 9908-014521 9908-014521 9908-014521 9908-014521 9908-014521 9908-014521 9908-014521 9908-014521 9908-014521 9908-014521 9908-014521 9908-014521 9908-014730 9908-014872 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-015106 9908-0155459 9908-0155459 9908-0155459 9908-015803 9908-015803 9908-015803 9908-015803 9908-015803

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RESULT :
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including:
allergies,
                    The present sequence is the protein sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative, autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification,
                                                                                                                                                                                                                                                          Hillman
Azimzai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                               Novel transcription factor polypeptides, used to treat diseases associated with altered activity and expression of TRFX, and to for agents capable of modulating its activity - \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; transcription factor; TRFX; cell proliferative disease; autoimmune disease; inflammation; neurological disease; developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2001
                                                                                                                         Claim
                                                                                                                                                                                                       N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABB57737-ABB72072)
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                                                                                                                       Pages 161-162;
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               arteriosclerosis,
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Bandman
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  asthma,
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P, Au-Young
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             AIDS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays protein
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990S-0130077

990S-0130110

990S-0130110

990S-0131449

990S-0132447

990S-0132485

990S-0132486

990S-0132486

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990S-0132487

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990S-0134218

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990S-0134211

990S-0134211
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99US-0127462.
99US-0128234.
99US-0128714.
99US-0129845.
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75.0%;
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05-MAR 1999

09-MAR 1999

23-MAR-1999

25-MAR-1999

10-APR-1999

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23-APR-1999

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9908-0125788
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9908-0128734
9908-0129045
9908-0130047
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71.4%;
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114-JUN 1999
116-JUN 1999
116-JUN 1999
117-JUN 1999
118-JUN 1999
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990S-0138540
990S-0139452
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990S-014180
990S-0142184
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990S-0144814
990S-0145284
990S-014730
990S-0147204
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990S-0147204
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pathway;
promoter;

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Query Match
Best Local S
Matches 5
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24-AUG-1999
27-AUG-1999
28-COT-1999
28-COT-1999
29-COT-1999
21-OCT-1999
22-OCT-1999
23-OCT-1999
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                   Similarity
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990S-0148341
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990S-0149368
990S-0149722
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990S-0151066
990S-0161066
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990S-0161061
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                    2;
                  Score 30; DB 21;
Pred. No. 3e+02;
2; Mismatches
                    0;
                                     Length 395;
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                    0,
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16-APR-1999
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9908-0130510
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RESULT 15
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Matches 5
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25-AUG-1999
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28-SEP-1999
29-SEP-1999
20-SEP-1999
21-OCT-1999
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                                                                             Similarity
5; Conserv
 standard;
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9905-0149723
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9905-0151065
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9905-0151303
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 Protein;
                                                                                         78
71
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                                                                               Score 30; DB Pred. No. 3.2e 2; Mismatches
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3.2e+02
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                                                                                                 Length
                                                                                 Indels
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18-JUN 1999
11-JUN 1999
22-JUN 1999
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17-NOV-2000
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08-DEC-2000
08-DEC-2000
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06-SEP-2000

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25-SEP-2000

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13-OCT-2000

08-NOV-2000

08-NOV-2000

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                                         The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM42347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
isolated from a range of human the nucleic acids, proteins, and in the diagnosis, treatment and
                                                                                                                                                                       Claim 11;
                                                                                                                                                                                                              Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorde
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                                                                                                                                                               ID NO 117; 532pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SCI INC
                                                                                                                                                                                                                                                                                                                                                                                        Ruben
antibodies and (ant)agonists are useful and prevention of: (a) cancer, e.g. brea
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Query Match
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Matches 6
                                                                                                                                                                                                                                                                                              and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direction WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                      Local Similarity
nes 6; Conser
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SRDTEVL 8
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85.7%;
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Search completed: August 31, 2002, 12:15:26 Job time: 232 sec

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US-08-806-263-2
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US-08-167-919A-11
US-08-167-15-106-11
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US-08-163-102-4
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US-08-884-154-4
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| , 1 5 324 | Query M Best Lo Matches | O B N I N | RESULT 1 US-08-854-5; Sequence; Patent No; GENERAL APPLIC | 2000 2000 2000 2000 2000 2000 2000 200 |
| 2 | <pre>y Match Local Similarity 100.0%; Score 38; DB 3; Local Similarity 100.0%; Pred. No. 3; nes 8; Conservative 0; Mismatches 0;</pre> | LE OF INVENTION: Density Enhanced Protein BER OF SEQUENCES: DDRESSE: Marshall, O'Toole, Gerstein, Mur DDRESSEE: Marshall, O'Toole, Gerstein, Mur TREET: 233 South Wacker Drive, Suite 6300 ITY: Chicago TATE: Illinois OUNTRY: United States of America IP: 60606 PUTER READABLE FORM: PUTER READABLE FORM: EDJUM TYPE: Floppy disk OMPOTER: IBM PC compatible PERATING SYSTEM: PC-DOS/MS-DOS OFTWARE: Patentin Release #1.0, Version #1 RENT APPLICATION DATA: PPLICATION NUMBER: US/08/854,585 ILING DATE: OR APPLICATION DATA: PPLICATION NUMBER: US/08/237,940 PLICATION NUMBER: 25,447 EGISTRATION NUMBER: 25,447 EFERENCE/DOCKET NUMBER: 27866/31954 ECCOMMUNICATION INFORMATION: ECCOMMUNICATION INFORMATION: ELEPHONE: 312-474-0448 MAPTION FOR SEQ ID NO: 2: UENCE CHARACTERISTICS: ENGTH: 1337 amino acids SYPE: amino acids OPOLOGY: linear ECULE TYPE: protein 4-585-2 | ALIGNMENTS 85-2 2, Application US/08854585 INFORMATION: ANT: Tonks, Nicholas K. and stman, Arn | 26 68.4 201 1 US-07-929-580B-5 26 68.4 223 1 US-07-708-885B-3 26 68.4 223 1 US-07-708-885B-3 26 68.4 223 1 US-07-708-885B-3 26 68.4 422 3 US-07-708-884-3 26 68.4 434 2 US-08-944-154-2 26 68.4 434 2 US-08-916-192A-2 26 68.4 447 2 US-08-912-192A-2 26 68.4 650 1 US-08-121-713D-60 26 68.4 650 1 US-08-835-268-60 26 68.4 650 2 US-09-060-692-60 26 68.4 650 3 US-09-060-692-60 26 68.4 650 3 US-09-060-610-60 26 68.4 650 4 US-09-060-610-60 26 68.4 650 5 PCT-US94-1015IA-60 27 68.4 1462 3 US-07-92-601-31 28 68.4 1462 3 US-07-92-601-31 29 68.4 1462 3 US-07-135-31 |
| | Length 1337; Indels 0; Gaps 0; | Tyrosine Phosphatase | | Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 142, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 60, Appli Sequence 31, Appli |
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; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-387-695-2
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Way, Earl
APPLICANT: Warnen, Stephanie
APPLICANT: Warren, Patrick V.
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: done
FILE REFERENCE: GM10237
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; Sequence 2, Application US/09387695
; Patent No. 6280990
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GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
                                                                                                            SEQ ID NO 2
LENGTH: 1042
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Best Local Similarity
Matches 8; Conserv
Query Match
                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/387,695 CURRENT FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 SOFTWARE: FastSEQ
                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447 REFERENCE/DOCKET NUMBER: 27/ TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Borun, Michael F.
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
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SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No.
76.3%;
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Length 1042;

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Matches 6; Conservative
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CURRENT APPLICATION NUMBER: US/09/172,977
CURRENT FILING DATE: 1998-10-14
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1336 RSRDVEVL 1343
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                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                          CITY: Gainesville
                                                                                                                                                                                                                                                                                                        STREET:
APPLICATION NUMBER:
                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                      Florida
Y: U.S.A.
                                                                                                                                                                                                                                                                                                        E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.3%;
75.0%;
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                                                 US 07/908,241
US 07/908,630
                                                                                                                   US/08/307,499
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Pred. No. 4
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4.2e+02
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FILING DATE: 29 CLASSIFICATION:

29-JUN-1992

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Best Local S
Matches 5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                             APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus
TITLE OF INVENTION: Live Vaccine Vector
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 904-372-5800
                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US 07/342,212 FILING DATE: 21-APR-1992 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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nes 5; Conserv
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83.3%;
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Pred. No.
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Best Local Similarity
""thes 5; Conserve
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; MOLECULE TYPE: protein US-08-356-405-2
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Patent No. 5807691
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                                                                                                     TELEFAX: (610)454-380
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UF TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                              SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
                                                                                                                                                                                                                     APPLICATION NUMBER: FR 92/08081 FILING DATE: 01-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO POFILING DATE: 29-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hen, Rene
APPLICANT: Plassat, Jean-Luc
TITLE OF INVENTION: Polypepti
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Polypepti
                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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LENGTH: 75 amino acids
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                               TYPE: ami
                                                                                                                                                                                      NAME: Smith, Julie K REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 500 Arcola CITY: Collegeville
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                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/356,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19426-0107
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                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boschert,
                                                                                                                   (610)454-3839
(610)454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Boschert, Ursula
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                                   linear
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83.3%;
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                                                                                                                                                                                   38,619
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Pred. No. 20;
1; Mismatches
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20;
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                                                                        US-08-969-815-4
                                                                                       RESULT
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Best Local Similarity
""" hes 6; Conserv
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Best Local Similarity
6; Conserv
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                                          Sequence 4, Application US/08969815 Patent No. 6207412
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                              GENERAL INFORMATION:
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APPLICANT: Sathe, Gan
APPLICANT: Van Horn,
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CDNA (
TITLE OF INVENTION: A NO. 
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: SmithKline B
STREET: 709 Swedeland R
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
NPDT TOATTON NUMBER: US/08/806,263
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                   332 SRDTEEL 338
                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
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CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 24-FEB-1997
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linear
Witte, Owen N. Weng, Zhigang
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cDNA Clone HDPBI30 That Encodes
A No. 6221627el Human 7-Transmembrane Receptor
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75.0%;
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Pred. No.
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                                                                                                                                                                                                                      Length 371;
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Best Local Similarity
Thehes 6; Conserva
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; FRAGMENT TYPE:
US-08-969-815-4
                                                                                                                                                                                                                                                                                                                                                   US-09-120-025-4
                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09120025 Patent No. 6214562
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 380 amino acid
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Bartteld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: UC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             TITLE OF INVENTION: TRANSCRIPTIONALLY REGULATED G PROTEIN-COUPLED TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                           APPLICANT: Weng, Zhigang. APPLICANT: Witte, Owen N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                        341 SRDTEEL 347
                                                                                    COUNTRY: U.
ZIP: 92660
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                      CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive, 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                      U.S.A.
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1in MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bartfeld, Neil S
REGISTAGN NUMBER: 39,901
REFERENCE/DOCKET NUMBER: UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/969,815
FILING DATE: 13-NOV-1997
                           PRIOR APPLICATION DATA:
                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WILKINSON, DAVID TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE TITLE OF INVENTION: AND USE THEREOF NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341 SRDTEEL 347
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                APPLICATION NUMBER: FILING DATE: 12-DEC
                                                                                                                                                FILING DATE: 18-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 6; Conserv
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                 APPLICATION NUMBER:
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5. 5674691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boyd, Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ward, Larry D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simpson, Richard
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internal
                                                12-DEC-1991
19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.1%;
85.7%;
                                                            PK9992 (AU)
                                                                                                                                                                             US/08/167,919A
                 PCT/AU92/00294
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2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 380;
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US-08-715-106-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTUDANCE

NAME: DIG191-
REGISTRATION NUMBER: 9100
REFERENCE/DOCKET NUMBER: 9100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                     APPLICATION NUMBER: 08/167
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                 APPLICATION NUMBER: I
FILING DATE: 12-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                   FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTO
TITLE OF INVENTION: AND USE THEREOF
              REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 SRDDEVL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Garden City
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                                                                 DiGiglio, Frank S.
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linear
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(516)
                                                                                                                                                          12-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.18;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Richard J.
                                                                                                                                                                         PK9992 (AU)
                                                                                                                       PCT/AU92/00294
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Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR-TYPE TYROSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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TELEFAX:

(516) 742-4366

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-715-106-11
                                                                                                     US-08-914-999-12
                                                                                                                      RESULT
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                                                Sequence 12, Application Patent No. 6346406
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Zalkin, Howard
APPLICANT: Smith, Janet L.
                                                                                                                                                                                                                                                         Query Match
Best Local
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CURRENT FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Switzer, Robert L.
TITLE OF INVENTION: DEREGULATION OF GLUTAMINE PRPP AMIDOTRANSFERASE
TITLE OF INVENTION: ACTIVITY
FILE REFERENCE: 3220-60979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Bacillus subtilis
ORGANISM: Bacillus subtilis
PUBLICATION INFORMATION:
AUTHORS: Makaroff, Christopher A.
AUTHORS: Zalkin, Howard
AUTHORS: Voltzer, Robert L.
AUTHORS: Vollmer, Steven J.
AUTHORS: Vollmer, Steven J.
TITLE: Cloning of the Bacillis Subtilis Glutamine
TITLE: Phosphoribosylpyrophosphate Amidotransferase Gene
TITLE: Escherichia Coli
                                                                                                                                                                                                                                                                                                                                      ISSUE: 17
PAGES: 10586-10593
DATE: 1983-09-10
                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL: J.
VOLUME: 258
APPLICANT:
               APPLICANT:
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                                                                                                                                                                       125
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                                                                                                                                                                                                                                      Local Similarity 85.7 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                       SSDTEVL 131
                                                                                                                                                                                                     SRDTEVL 8
                                                                                   Application US/08914999
                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem
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               Ryazanov, Alexey G.
Hait, William N.
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Pavur, Karen S
                                                                                                                                                                                                                                                         71.1%;
85.7%;
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85.7%;
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                                                                                                                                                                                                                                                       Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                         US-08-914-999-10
                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ryazanov, Alexey
APPLICANT: Hait, William N.
APPLICANT: PAVUE, Karen S.
TITLE OF INVENTION: ELLONGAT
TITLE OF INVENTION: AND MET
                                                                                                                                                                                                                                                                                                                          Sequence 10, Appli
Patent No. 6346406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ANAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: pro
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
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ORIGINAL SOURCE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentLn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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STATE: New Jersey
                                                                                                             CITY: Hackensack
STATE: New Jersey
                                                                                                                                             STREET: 411 Ha
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STRANDEDNESS: si
                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                        3: David A. Jackson, Esq.
411 Hackensack Ave, Continental Plaza, 4th
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Hait, William N.
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PatentIn Release #1.0, Version #1.30
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Pred. No.
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CURRENT APPLICATION NUMBER: US/OB/914,999
FILING DATE:
CLASSIFICATION: 435
APTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/DOCCET NUMBER: 601-1-078
FELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 anino acids
TYPE: anino acids
TYPE: maino acids
TYPE: protein
CHECOLLE TYPE: protein
HYPOTHETICAL: NO
ONIGINAL SOURCE:
ORGANISM: C. elegans
US-08-914-99-10

OUCRY Match
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
MATCHES 5: Conservative 1; Mismatches 0; Indels 0; Gaps
MATCHES 5: Conservative 1; Mismatches 0; Indels
OY 1 QSEDTE 6
Db 476 QTEDTE 481

Search completed: August 31, 2002, 12:15:45
Job time: 141 sec
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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Match
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Compugen Ltd.
O9npr5 homo sapien Q15255 homo sapien Q15255 homo sapien O940h7 mus musculu O60140 schizosacch Q9szz6 arabidopsis Q97qa6 straptococc Q9bak0 lepidothamn Q33236 tradescanti Q9bct8 homo sapien Q9w2r1 drosophila Q9hb58 homo sapien Q9hb58 homo sapien Q91404 xenopus lae Q46025 corynebacte Q90m04 human immun Q9u247 caenorhabdi
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| Q9xu14 c Q9bai3 p Q9by66 Q9bu59 p Q9bu59 p Q9bu59 p Q9bu51 p Q9d1i8 Q9jj70 Q99m63 p Q957612 Q957612 Q957612 Q944m7 c Q9sb74 P7240 s Q9sb74 P7240 s Q9su91 |
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ALIGNMENTS

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                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 human gene transcripts.";
Submitted (JUN-2000) to the EMEMBL; AL359057; CAB94390.1; -.
InterPro: IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 2.
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Q9NPR5;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTPRJ, PROTEIN TYROSINE PHOSPHATASE RECEPTOR J, ETA
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                       Receptor.
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SEQUENCE
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Andreu N., Estivill J
Submitted (JUN-2000)
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Lehrach H., Poustka A., Lundebe
"The European IMAGE consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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324 QSRDTEVL
                                                            1 QSRDTEVL
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Lundeberg J.
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a novel protein-tyrosine phosphatase, HPT Blood 84:4186-4194(1994).
EMBL; D37781; BAA07035.1; -.
HSSP; P18052; 1YFO.
InterPro; IPR001395; Aldo_ket_red.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00041; fn3; 5.
Pfam; PF00041; Y_phosphatase; 1.
[1]
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
STRAIN-C5BL/6J; TISSUE-EMBRYO;
STRAIN-C5BL/6J; TISSUE-EMBRYO;
STRAIN-C5BL/6J; TISSUE-EMBRYO;
STRAIN-C5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9D0H7 PRELIMINARY;
Q9D0H7;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
2610016F07RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q15255 PRELIMINARY; PRT; 133
Q15255;
Q1-NOV-1996 (TremBLrel. 01, Created)
Q1-NOV-1996 (TremBLrel. 01, Last sequen
Q1-DEC-2001 (TremBLrel. 19, Last annota
PROTEIN-TYROSINE PHOSPHATASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSIT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00063; ALDOKETO_REDUCTASE_3; PROSITE; PS00383; TYR_PHOSPHATASE_1; 1. PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00700; PRTYPHPHTASE. SMART; SM00060; FN3; 6. SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POV1 OR 2610016F07RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=95086212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Honda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
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19 38 POTENTIAL.
971 995 POTENTIAL.
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971
1337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331
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Primates;
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osine phosphatase,
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Pred. No. 4.4
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Ve
Catarrhini;
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annotation update)
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Peta.";
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RESULT Q9SZZ6
ID Q9SZZ6
AC Q1
DT 01
DT 01
DT 01
DT 01
DT 01
CON H1
CON L1
OS A1
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Best Local S
Matches 7
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Best Local Similarity
Matches 6; Conser
          Q9SZZ6

Q9SZZ6;
Q9SZZ6;
01-MAY-2000 (TIEMBLrel. 13, Creation Core. 13, Last Ol-CCT-2000 (TIEMBLrel. 15, Last Ol-CCT-2000 (TIEMBLrel. 15, Last HYPOTHETICAL 27, 8 KDA PROTEIN. L73G19.60 OR AT4G25680.

L73G19.60 OR AT4G25680.

Arabidopsis thaliana (Mouse-ear Arabidopsis thaliana (Mouse-ear Core. 15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quaraction, Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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060140;
01-AUG-1998
01-AUG-1998
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TIEMBLIER) 07, Created)
01-AUG-1998 (TIEMBLIER) 07, Last sequence update)
01-OCT-2000 (TIEMBLIER) 15, Last annotation update)
HYPOTHETICAL 49.1 KDA PROTEIN.
SPBC18H10.09.
SCHIZOSACCHAROMYCES pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                         Lyne M., Rajandream M.A., Ba
Submitted (MAR-1998) to the
EMBL; AL022304; CAA18406.1;
                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK011417; BAB27605.1; -.
MGD; MGI:1931352; POV1.
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Kuehl P., L
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
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"Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 SRDTEVL
                                                                                                                                                                                     150 QSKDTELL 157
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 Viridiplantae;
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428 AA; 4
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                                                                                                                                                                                                                                            Conservative
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              (Mouse-ear
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75
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he EMBL/GenBank/DDBJ databases.
1; -.
se-ear cress).
Streptophyta;
                                                      Last sequence update)
Last annotation update)
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Pred.
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Pred. No.
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Nikaido I., Pesc
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                                                                                                                                                                                                                                           Mismatches
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No.
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35;
Embryophyta;
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32;
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 Tracheophyta;
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       Matches
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Q97QA6;
Q97QA6;
01-OCT-2001 (TremBLrel. 18, C
01-OCT-2001 (TremBLrel. 18, L
01-DEC-2001 (TremBLrel. 19, L
V-TYPE SODIUM ATP SYNTHASE, S
                                                                                                                                                                                                                                                Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bevan M.,
Mayer K.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/G
EMBL; AL050400; CAB43599.1; -
EMBL; AL151563; CAB81378.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702;
                                                                                                                    SEQUENCE 335 AA
                                                                                                                                                                    TIGR; SP1319;
                                                                                                                                                                                       Science 293:498-506(2001).
EMBL; AE007430; AAK75417.1;
                                                                                                                                                                                                                                    pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-TIGR4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
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    Similarity
6; Conserv
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'X., Schueller C.;
(MAY-1999) to the EMBL/G
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       Conservative
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Clostridium
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                                                                                                                    MW;
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       1;
Score 31; DB Pred. No. 46; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
SUBUNIT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
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                                                                                                                    5825DBF919EFD405
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                                               Length 335;
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Best Local
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Q33236 PRELIMINARY; PRT;
Q33236;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 19, Last sec
O1-DEC-2001 (TREMBLREL. 19, Last and
RIBULOSE BISPHOSPHATE CARBOXYLASE LA
LARGE SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = PHOSPHO-D-GLYCERATE.
-!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
-!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
EMBL; AF445042; AAK29524.1; -.
HSSP; P04718; 1RUS. RUBISCO large.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chloropiast gene rbci.";
Aust. Syst. Bot. 0:0-0(2000).

Aust. Syst. Bot. 0:0-0(2000).

FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION THE PENTOSE SUBSTRATE IN THE PHOTORESFIRATION PROCESS. BOTH REACTIONS OCCUR SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE (BY SINULTANEOUSLY AND IN COMPETITION AT THE SAME ACTIVE SITE OF SITULTANEOUSLY AND SITULTANEO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9BAKO;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN (EC 4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00157; RUBISCO_LARGE; 1. Carbon dioxide fixation; Chloroplast; Oxidoreductase; Photorespiration; Pho
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446 AA;
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Coniferopsida; Coniferales;
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62.5%;
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                                   Last sequence update)
Last annotation updat
XYLASE LARGE CHAIN (EC
                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P.G., Dowd J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1FB6045EE477F236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyase; Monooxygenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
62;
                                   tion update)
CHAIN (EC 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quinn
                                          4.1.1.39) (RUBISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G
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RESULT
Q95CG3
DT 00
DT 00
OC 0
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O95CG3
O95CG3
C 095CG3;
JT 01-DEC-2001 (TrEMBLrel. 19, Last sc., DT 01-DEC-2001 (TrEMBLrel. 19, Last annotate DT 01-DEC-2001 (TrEMBLrel. 19, Last annotate LAI "TRULOSE 1,5-BISPHOSPHATE CARBOXYLASE LAI "TRULOSE 1,5-BISPHOSPHATE CARBOXYLASE LAI "Thuta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Phylogenetic analysis of the Zingiberales using rbcl sequence data.";

Lubmitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.

C -I- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-

RIBUJOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC

C RIBUJOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC

C CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF

THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH

C REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME

C ACTIVE SITE (BY SIMULTANEOUSLY AND IN COMPETITION AT THE SAME

C -I- CATALYTIC ACTIVITY: D-RIBUJOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-

C PHOSPHO-D-GLYCERATE + 2-PHOSPHOGED 1,5-BISPHOSPHATE + O(2) = 3-

PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

-I- SUBCELULIAR LOCATION: CHLOROPLAST (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 5
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00016; RuBisCO_large; 1.
Pfam; PF02788; RuBisCO_large_N; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase; Oxidoreductase; Photorespiration; Photosynthesis.
                                              NON_TER
                                                                                                     Chloroplast.
                                                                                                                            EMBL;
                                                                                                                                                    Submitted (OCT-2000)
                                                                                                                                                                   JEQUENCE ..... Faden R.B., Givnish I.e. Evans T.M., Faden R.B., Givnish the "Phylogenetic Relationships in the "Phylogenetic Requence Data.";
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Pfam; PF02788; RuBisCO_large_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: CHLOROPLAST (
-i- SIMILARITY: BELONGS TO THE RUBISCO EMBL; L05463; AAA98393.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith J.F., Kress W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae;
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                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                               Tradescantia
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                                                                                                                          AF312238; AAL26157.1;
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5; Conservative
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456
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                                                                                                                                                 Sequence Da
                    456
50570 MW;
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62.5%;
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/ta; Liliopsida; Commelinales; Commelinaceae;
                                                                                                                                                                                                                                                                                                                                                                              Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB Pred. No. 63; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
ARBOXYLASE LARGE SUBUNIT (FRAGMENT).
                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                      Liliopsida;
                       13477E0E231F0440 CRC64;
                                                                                                                                                                                                                          T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FD6D70BF80D239B0 CRC64;
                                                                                                                                                                                                  J., Sytsma K.J.; Commelinaceae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456
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                                                                                                                                                                                                                                                                                                                                                                              Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                         Commelinales;
                                                                                                                                                                                                                          К.J.;
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RE SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RE STRAIN-BERKELEY;

RX MEDLINE-20196006; PubMed-10731132;

RX MEDLINE-20196006; PubMed-10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Wan K.H., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Pallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Pallew R.M., Basu A., Bareman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q9HCT8
                                        Q9W2R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HCT8;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9W2R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclear hormone receptor transcriptional coactivator. Mol. Cell. Biol. 20:6138-6146(2000). EMBL; AF280094; AAF99318.; -...
Interpro; IPR000770; SAND. SAND; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, TRANSCRIPTIONAL COACTIVATOR HOMO SERIOS (""----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG9993 PROTEIN.
CG9993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bloch D.B., Nakajima A., Gulick T., Chiche J.D., Orth D., de La Monte S.M., Bloch K.D.; "Spil0 localizes to the PML-Spi00 nuclear body and may function
                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9W2R1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                             Neoptera; Endopterygota; Diptera;
); Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Arthropoda; Tracheata; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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ima A., Gulick T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60760 MW;
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62.5%;
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75.0%;
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13,
17,
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Last sequence update)
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Last annotation updat
SP110B.
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Pred. No.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft G., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF280095; AAG09826.1; ~. InterPro; IPR001487; Bromodomain.

InterPro; IPR001955; PHD.

InterPro; IPR000770; SAND.
Pfam; PF00628; PHD; 1.
SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                  Bloch D.B., Nakajima A., de la Monte S.M., Bloch I
                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                     TRANSCRIPTIONAL COACTIVATOR
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Cherry J.M., Cawley S.
de Pablos B., Delcher
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InterPro; IPR000508; Peptidase_S26.
Pfam; Pr00501; AMP-binding; 1.
PROSITE; PS00761; SPASE_I_3; 1.
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                                                                                                                                                                                                                                                              Primates;
                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60344 MW;
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Sp110.
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Pred. No.
                                                                                                                                                                                                                                                             Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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77;
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Fleischmann W.,
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Smith H.O.,
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Query Match
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Best Local
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01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                  Q46025
Q46025;
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Q91404;
MEDLINE-95286547; PubMed-7768861;
Tai S.S., Zhu Y.Y.;
"Cloning of a Corynebacterium diphtheriae iron-repressible gene that
shares sequence homology with the AhpC subunit of alkyl hydroperoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-95290493; PubMed-7772598;

MEDLINE-95290493; PubMed-7772598;

Adati N., Ito T., Koga C., Kito K., Sakaki Y., Shiokawa K.;

"Differential display analysis of gene expression in develor

"Bisochim. Biophys. Acta 1262:43-51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XK ENDO B HOMOLOG PROTEIN (FRAGMENT).
XK ENDO B HOMOLOG.
XK ENDO B HOMOLOG.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
Amphibia; Batrachia; Anura; Mesobatrachi
                                                                              Actinomycetales;
Corynebacterium.
NCBI_TaxID=1717;
                                                                                                                  Corynebacterium diphtheriae. Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                           DIRA.
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                                                STRAIN=C7
                                                         SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00226; IF; 1.
Coiled coil; Intermediate filament.
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InterPro; IPR001664; IF.
Pfam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae;
                                                                                                                                                    IRON REPRESSIBLE POLYPEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                 105 AA; 11896 MW; CDD924315223514A CRC64;
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75.08;
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Pred. No.
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Pred.
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No.
                                                                                                       Corynebacteriaceae;
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                                                                                                                   Actinobacteridae;
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99;
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23;
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expression in developing
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ia; Pipoidea; Pipidae;
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RESULT 15

Q90M04

ID Q90M04;
AC Q90M04;
DT 01-DEC-2001 (TIEMBLIE1. 19, Created)
DT 01-DEC-2001 (TIEMBLIE1. 19, Last sequence update)
DT 01-DEC-2001 (TIEMBLIE1. 19, Last sequence update)
DT 01-DEC-2001 (TIEMBLIE1. 19, Last sanotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Human immunodeficiency virus type 1.

Viruses; Retroid viruses; Retroviridae; Lentivirus.

OK VIRUSES; Retroid viruses; Retroviridae; Lentivirus.

OK NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=WM1014;
RA Herring B.L., Dwyer D.E.;
RI "Australian HIV-1 env subtypes.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF400083; AAK91742.1; -.

FT NON_TER 218 218
SQUENCE 218 AA; 24303 MW; EBF49BA240566450 CRC64;
Search completed: August 31,
Job time: 219 sec
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                                                                                                                                                                        Query Match 78.9
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Herring B.L., Dwyer D.E.;
"Australian HIV-1 env subtypes.";
submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF400083; AAK91742.1; -.
NON_TER 1 1
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SEQUENCE 218 AA; 24303 MW; E8F49BA240566450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reductase of Salmonella typhimurium.";

J. Bacteriol. 177.3512-3517(1995).

EMBL; U18620; AAA96946.1; -.

InterPro; IPR000866; AhpC-TSA.

Pfam; PF00578; AhpC-TSA; 1.

SEQUENCE 198 AA; 22312 MW; 7A09DCB4A07705DD CRC64;
                                                                                              1 QSRDTEV 7 :||||: 198 ESRDTEI 204
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ALIGNMENTS

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RESULT 1
PTPJ_HUMAN
                     InterPro; IPR00
InterPro; IPR00
Pfam; PF00041;
                                                                                                   EMBL; U10886;
EMBL; D37781;
HSSP; P18052;
MIM; 600925; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95086212; PubMed-7994032; Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.; "Molecular cloning, characterization, and chromosomal localization a novel protein tyrosine phosphatase, HPTP eta."; Blood 84:4186-4194(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTPJ_HUMAN STANDARD; PRT; 1337 AA.

012913; 015255;

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Protein tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
(HPTP eta) (Density enhanced phosphatase-1) (DEP-1) (CD148 antigen).
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                               -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

tyrosine + phosphate.
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- PTM: N- AND O-GLYCOSYLATED.
-I- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
-I- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- DATABASE: NAME=PROW; NOTE=CD guide CD148 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-95024024; PubMed=7937872;

MEDLINE-95024024; PubMed=7937872;

MEDLINE-95024024; PubMed=7937872;

MEDLINE-95024024; PubMed=7937872;

MEDLINE-95024024; Proceedings of the protein-tyrosine-phosphatase, percentage of the protein-tyrosine-phosphatase, is enhanced with increasing cell density.";

Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       InterPro; IPR003961; FN_III.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_prot_phphtase.
Pfam; PF00041; fn3; 5.
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PF00102; Y_phosphatase;
                                                                                                                                                                                                       email to license@isb-sib.ch).
                                                                                                                          IYFO.
                                                                                                                                           AAB36687.1;
BAA07035.1;
                                                                                                                                                                                                                          license agreement (See http://www.isb-sib.ch/announce/
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RESULT 2
YG44_SCHPO
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
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                                                                                                                                                                                    OSRDTEVL 331
                                                                                                                                                                                                           QSRDTEVL 8
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SM00194; PTPC;
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  (Rel.
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454
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                                                                      STANDARD;
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BY SIMILARITY.
N-LINKED (GLCNAC.
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                                                                      PRT;
                                                                                                                                                                                                                                                                                                  Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR
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    update)
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GILCNA
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N TYPE-III 1.
N TYPE-III 2.
N TYPE-III 3.
N TYPE-III 4.
N TYPE-III 5.
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                                                                                                                                                                                                                                                                                                                       Length 1337;
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(POTENTIAL).
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Best Local S
Matches 6
                                                                                                                                                          STRAIN-VF5;

MEDLINE-98196666; PubMed-9537320;

Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenv
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M
Graham R.A., Short J.M., Olson G.J., Swanson R.V.;

Feldman R.A., Short J.M., hvberthermophilic bacterlum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50077; HEAT_REPEAT; 1.

Hypothetical protein.

REPEAT 1600
        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        YC11_AQUAE
067264;
                                                                                                                                                                                                                                                                                                                                                                                                                 LT 3
_AQUAE
                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wood V., Rajandream M.A., Barrell B.G., Pohl Submitted (MAY-1998) to the EMBL/GenBank/DDBJ-i-SIMILARITY: BELONGS TO THE BAP28 FAMILY.
                                                                                                                                                aeolicus.
                                                                                                                                                                                                                                                                         Aquifex aeolicus.
Bacteria; Aquificales;
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical 186.4 kDa protein C23E6.04c in c SPBC23E6.04C.
                                                                                                                                                                                                                                                                                                                    Hypothetical AQ_1211.
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                                                                                                                    -!- SIMILARITY: TO A.AEOLICUS
                                                                                                                                    Nature
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                    392:353-358(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
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(Rel. 40,
(Rel. 40,
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(Rel. 40, Last an
protein AQ_1211.
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                          Aquificaceae; Aquifex
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                                                                                                                                                                                                                                                                                                                                              sequence update)
annotation update)
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Pred. No. 71;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                    AQ_820 AND AQ_1583.
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                        (See http://www.isb-sib
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ay M.,
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  Matches
                   Query Match
Best Local 9
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Best Local
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Hypothetical
SEQUENCE 20
                                                                                                  Prodm; PF00275; EPSP_Syntase; 1.
ProDom; PB001867; EPSP_SYntase; 1.
PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
PROSITE; PS00885; EPSP_SYNTHASE; 2; 1.
Aromatic amino acid biosynthesis; Transferase; CSEQUENCE 430 AA; 44557 MW; 445975BA53DC74D9
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N. Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9CCI3;
Q9CCI3;
Q1-MAR-2002 (Rel. 41, Created)
Q1-MAR-2002 (Rel. 41, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC enolpyruvylshikimate-3-phosphate synthase) (EPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-i- CATALYTIC ACTIVITY: Phosphoenolpyruvate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                     EMBL; AL583919; CAC30301.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AROA OR ML0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AROA_MYCLE
                                                                                                                                                                                                                            InterPro; IPR001986; EPSP_syntase
                                                                                                                                                                                                                                           Leproma; ML0792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MONOMER (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate phosphate + 5-0-(1-carboxyvinyl)-3-phosphoshikimate. PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||:|||
QKRDSEVL 78
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                                                                                                                                                                                                       PF00275; EPSP_syntase;
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Similarity
5; Conserv
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6; Conservative
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  Conservative
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62
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75.0%;
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Score 29; DB Pred. No. 43; 3; Mismatches
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Pred. No. 11;
1; Mismatches
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11;
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synthase)
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RESULT 5
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01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-phosphoshikimate 1-carboxyvinyltransferase (EC enolpyruvylshikimate-3-phosphate synthase) (EPSP AROA OR RV3227 OR MT3324 OR MTCY20B11.02.
                                                                                                            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91072223; PubMed=2123856; Garbe T., Jones C., Charles I.G., Dones C., Charles I.G., Dones T., Cloning and characterization of the
                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bishai W.;
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X52269; CAA36510.1;
M62708; AAA25356.1;
Z95121; CAB08328.1;
                                                                                        an email to license@isb-sib.ch).
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BELONGS TO THE EPSP SYNTHASE FAMILY.
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C Q29473; 002859;
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JT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
T 1-chrome P450 2D15 (EC 1.14.14.1) (CYPIID15) (P4
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                                                 MEDLINE-98162950; run....Ttoh S., Oha Tasaki T., Nakamura A., Itoh S., Oha Tasaki T., Kazusaka A., Kamataki T., Iwata H., Kazusaka A., Kamataki Oharacterization of
                                                                                                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
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ProDom; pD001867; EPSP_syntase; 1.

PROSITE; pS00104; EPSP_SYNTHASE_1; 1.

PROSITE; pS00885; EPSP_SYNTHASE_2; 1.

Aromatic amino acid biosynthesis; Transferase; Complete SEQUENCE 450 AA; 46425 MW; 27BB86F9412A07D5 CRC64;
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                        CHARACTERIZATION.
MEDLINE-98389575; PubMed-9721180;
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                                                                                                                                                                                                                                                                                                                   "A new cytochrome P450 for microsomes: purification, characterization.";
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InterPro; IPR001986; EPSP_syntase.
                                                                                                                                "Expression and characterization of canine Arch. Biochem. Biophys. 357:27-36(1998).
                                                                                                                                                       Tweedie D.J.;
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Takanaka A., Matsubara
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A37807.
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3; Mismatches
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome P450 2D16 (EC 1.14.14.1) (CYPIID
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15-DEC-1998
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                                                                                                                                                                                                                                                                                        "The gene sequence of
                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning and sequencing of a guinea pig cytochrome P4502D (CYP2D16): high level expression in adrenal microsomes."; Biochem. Biophys. Res. Commun. 209:1149-1156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Jiang Q., Voigt J.M., Colby H.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=13; TISSUE-Adrenal cortex;
MEDLINE-95251703; PubMed-7733969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
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                                                               ACIDS, AND XENOBIOTICS.

CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = Oxidized flavoprotein + H(2)O.

SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic retices specificity: Expressed at high Levels in the INN THE ADRENAL CORTEX.

SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
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Rodentia;
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of a xenobiotic metabolism-related
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Hystricognathi; Caviidae; Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on update) (CYPIID16).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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HE INNER ZONE
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                                    collaboration
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                      outstation
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Best Local S
Matches 6
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-I- FUNCTION: This protein is involved in the repair of mismatches in DNA. It is possible that it carries out the mismatch recognition step. This protein has a weak ATPase activity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                       InterPro; IPR000432; MutS_C.
InterPro; IPR002863; MutS_N.
Pfam; PP00488; MutS_C; 1.
Pfam; PP016624; MutS_N; 1.
ProDom; PD001263; MutS_C; 1.
                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99XL8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF020345; AAB94568.1; -.
Interpro; IPR001128; Cyt_p450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA mismatch repair MUTS OR SPY2148.
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Microsome; Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U21486; AAA68479.1; EMBL; AF020345; AAB94568.
                             SMART; SM00534; MUTSac; 1
SMART; SM00533; MUTSd; 1
                                                                                                                                 EMBL; AE006633; AAK34785.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / SEROTYPE M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21192684; PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382
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             PS00486; DNA_MISMATCH_REPAIR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
500 AA;
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446
123
127
ATP-binding; DNA-binding; Complete proteome
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446
123
127
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I -> V (IN REF. 2).
Y -> N (IN REF. 2).
G -> R (IN REF. 2).
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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51;
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ANK2_HUMAN
ID ANK2_H
AC Q01484
DT 01-APR
DT 16-OCT
DT 16-OCT
DE Ankyri
GN ANK2.
OS Homo s
OC Eukary
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Best Local
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                                                 ANK2_HUMAN STAN
Q01484; Q01485;
01-APR-1993 (Rel. 2
01-OCT-1996 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                     1267
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P48563;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.inhorsend.an email to licenseas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96132033; PubMed-8553702; Maurer K.C.T., Urbanus J.H.M., Planta R.J.; Maurer K.C.T., Urbanus J.H.M., Planta R.J.; Peguence analysis of a 30 kb DNA segment from yeast chromosome carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, a novel putative serine/threonine protein kinase gene."; Yeast 11:1303-1310(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update
Hypothetical 186.8 kDa protein in CLA4-PUS4
YNL297C OR N0453.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                        Ankyrin
                                                                                                                                                                                                                                                                                     Hypothetical SEQUENCE 16
                                                                                                                                                                                                                                                                                                              SGD;
                                                                                                                                                                                                                                                                                                                         EMBL; U23084; AAC49101.1; -. EMBL; Z71573; CAA96214.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=S288C / FY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                domo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QSRDTEVL 8
                                                                                                                                                                                             2 SRDTEVL 8
                                                                                                                                                                    SKDTEIL 1273
                                                                                                                                                                                                                                                                                                             S0005241; YNL297C.
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851 AA;
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                                                                                                      STANDARD;
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                            25, Created)
34, Last sequence update)
40, Last annotation update)
. 40, Last annotation update)
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Pred.
2; Mis
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Pred. No.
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; 737D51CBCDFEAF0A CRC64;
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95;
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                                                                                                                                                                                                                                   2e+02;
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                                         nonerythroid)
                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions on
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PRINTS; PRO1415; ANKYRIN.
SMART; SM00248; ANK; 21.
SMART; SM00005; DEATH; 1.
SMART; SM00015; DEATH; 1.
SMART; SM00218; ZU5; 1.
PROSITE; PS50018; ANK, REPEAT; 20.
PROSITE; PS50017; ANK, REP_REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                      EMBL; X56957; CAA40278.1; -. EMBL; X56958; CAA40279.2; -. EMBL; Z26634; CAB42644.1; -. EMBL; M37123; AAA62828.1; -. PIR; S14533; S14533. PIR; A39643; A39643.
                                                                                                     InterPro;
Pfam; PFO;
Pfam; PFO;
Pfam; PFO;
                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                            PIR;
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MEDLINE-92009921; PubMed-1833308;
MEDENER-92009921; PubMed-1833308;
Tse W.T., Menninger J.C., Yang-Feng T.L., Fra
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Attach integral membrane proteins to cytoskeletal elements. Also bind to cytoskeletal proteins.
-i- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL CELLS THROUGHOUT THE BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chan W., Kordeli E., Bennett V.;
"440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyelinated axons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Otto E., Kunimoto M., McLaughlin T., Bennett V.; "Isolation and characterization of cDNAs encoding ankyrins reveal a family of alternatively spliced J. Cell Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain stem;
MEDLINE-91302466; PubMed-1830053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; NCBI_TaxID=9606; [1]
                                                                                                                                                                 InterPro;
                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carpenter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell Biol. 123:1463-1473(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: PHOSPHORYLATED AT MULTIPLE SITES BY AND EACH PHOSPHORYLATION EVENT REGULATES AND FUNCTION (POTENTIAL).
SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                               106410; -
                                                                                                                                                                                                                            B39643; B39643.
S14569; S14569.
                                                                                                        PF00791;
                                                                                                                                      PF00023;
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                                                                                                                                               ; IPR002110; ANK.
; IPR000488; Death.
; IPR000906; ZU5.
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; death; 1.
; ZU5; 1.
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E., Bennett V.;
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                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamu Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T. Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., C Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechocystis sp. (strai
Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDXJ OR SLR1779
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"DNA sequence analysis of conserved and unique regions of swinepox virus: identification of genetic elements supporting phenotypic observations including a novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1148;
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                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                         PYRIDOXAL PHOSPHATE.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE PDXJ FAMILY.
                                                                                                                                                                                                                                                                                                          FUNCTION: CATALYZES THE CONDENSATION OF 1-DEOXY-D-XYLULOSE-5-PHOSPHATE (DXY) AND 1-AMINO-3-OXO-4-(PHOSPHOHYDROXY) PROPAN-2-ONE TO FORM PRILOXINE 5'-PHOSPHATE (PNP) (BY SIMILARITY).

PATHWAY: DE NOVO SYNTHESIS OF PYRIDOXINE (VITAMIN B6) AND
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P47694; Q49238;
01-FEB-1996 (Rel. 3
01-FEB-1996 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                   Fraser C.M., Cocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weldman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                    EMBL; U39727; I
EMBL; U39732; I
EMBL; U01790; I
TIGR; MG456; --
Hypothetical pi
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TRANSMEM
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or send an email to license@isb-sib.ch)
                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                    J. Bacteriol. 175:7918-7930(1993).
                                                                                                                                                                                                                                                                               sequencing.";
                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 86-182 FROM N.A. STRAIN=ATCC 33530 / G-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-ATCC 33530 /
                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                          "A survey of the Mycoplasma
                                                                                                                                                                                                                                                                                                     Peterson S.N.,
                                                                                                                                                                                                                                                                                                                MEDLINE=94075230;
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Similarity 6; Conser
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                                                                                                                                                                                                          non-profit institutions as long
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                                                                                                                                                                                                                                                                                                     30; PubMed=8253680;
Hu P.-C., Bott K.F.,
                                                          AA;
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38354
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75.0%;
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Pred. No. 54;
1; .Mismatches
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D142C358CE474C71 CRC64;
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4F9EBFD215C3876E CRC64;
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InterPro; IPROVA...
InterPro; IPROVA?; ig; 1.
Pfam; PF000429; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
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Glycopr
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P18466;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DLA class I histocompatibility antigen, A9/A9 alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of a dog class I cDNA clone.";
Immunogenetics 31:400-404(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90316611; PubMed=2370086;
Sarmiento U.M., Storb R.;
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Canis familiaris (Dog).
Cinis familiaris (Dog).
Cinis familiaris (Dog).
Cinis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                      249
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  STANDARD;
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207
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362
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62.5%;
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                    CONNECTING
   PRT;
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                                                                                                 Mismatches
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Best Local
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HSSP; P00876;
Mendel; 2897;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commen
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                                                                                                                                                                                                                                                                                                              Pfam; PF00016; RuBisCO_large; 1.
Pfam; PF02788; RuBisCO_large_N; 1.
PROSITE; PS00157; RUBISCO_LARGE; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Phylogenetics of seed plants: an analysis of nucleotide sequences from the plastid gene rbcL.";
Ann. Mo. Bot. Gard. 80:528-580(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ribulose bisphosphate carboxylase large chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Vir
Spermatophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION (THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE. SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS. SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phospho-D-glycerate.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY:
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OSRDTEVL
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IPR000685; RuBisCO_large.
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394
394 /
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Magnoliophyta; Liliopsida; Alismataceae; Alisma.
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                                                                            73.7%;
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